

APPENDIX A

BLAST**Basic Local Alignment Search Tool**

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[Edit and Resubmit](#) [Save Search](#) [Strategies](#) [Formatting options](#) [Download!](#)**SEQID40**Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
lcl|25193**Description**

SEQID40

Molecule type

amino acid

Query Length

597

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

ProgramBLASTP 2.2.24+ [Citation](#)**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#) [Multiple alignment](#)
[Search Parameters](#)**Search parameter name Search parameter value**

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Filter string	F
Genetic Code	1
Window Size	40
Threshold	11
Composition-based stats	2

Database

Database parameter name Database parameter value

Posted date	Sep 26, 2010 5:43 PM
Number of letters	4,071,357,309
Number of sequences	11,921,515
Entrez query	none

Karlin-Altschul statistics

Params Ungapped Gapped

Lambda	0.318492	0.267
K	0.132452	0.041
H	0.386991	0.14

Results Statistics

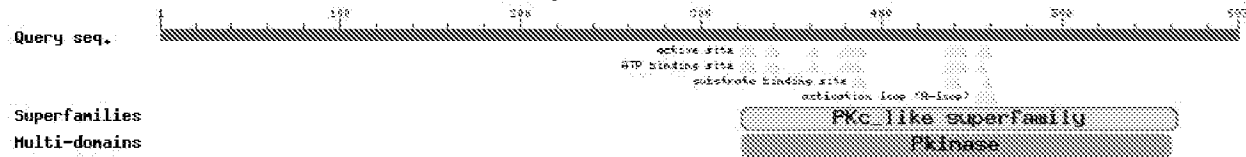
Results Statistics parameter name Results Statistics parameter value

Length adjustment	144
Effective length of query	453
Effective length of database	2354659149
Effective search space	1066660594497
Effective search space used	1066660594497

Graphic Summary

Show Conserved Domains

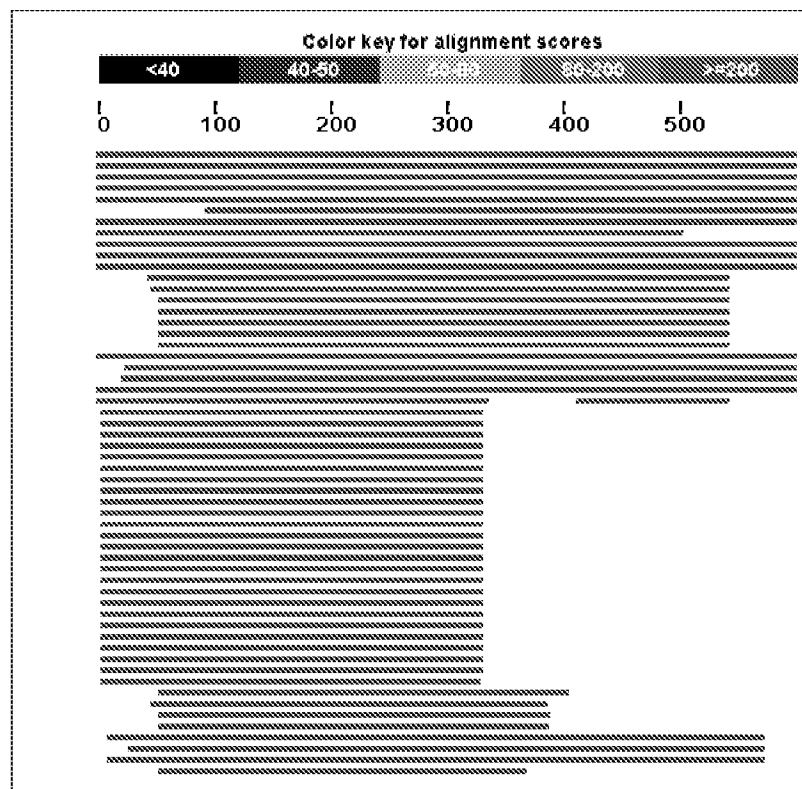
Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of 102 Blast Hits on the Query Sequence













[?]

















An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Descriptions

Legend for links to other resources:  UniGene  GEO  Gene  Structure  Map Viewer  PubChem BioAssay
Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Links
ABQ99609.1	NFR5a [Glycine max] >gb ADJ19105.1 Nod-factor receptor 5A [Glycine max] >gb ADJ19108.1 Nod-factor receptor 5A [Glycine max]	1058	1058	100%	0.0	
ADJ19108.1	Nod-factor receptor 5A [Glycine max]	1057	1057	100%	0.0	
ADJ19107.1	Nod-factor receptor 5A [Glycine max]	1055	1055	100%	0.0	
ADJ19112.1	Nod-factor receptor 5B [Glycine max]	1029	1029	100%	0.0	
ADJ19111.1	Nod-factor receptor 5B [Glycine max]	1028	1028	100%	0.0	
ABQ99613.1	NFR5b [Glycine max]	909	909	84%	0.0	
CAE02593.1	SYM10 protein [Pisum sativum] >emb CAE02594.1 SYM10 protein [Pisum sativum]	870	870	100%	0.0	
ADJ19110.1	truncated Nod-factor receptor 5A [Glycine max]	866	866	83%	0.0	
CAE02595.1	SYM10 protein [Pisum sativum] >emb CAE02596.1 SYM10 protein [Pisum sativum] >gb ADB45277.1 Nod factor recognition protein [Pisum sativum]	865	865	100%	0.0	
CAE02597.1	Nod-factor receptor 5 [Lotus japonicus] >emb CAE02598.1 Nod-factor receptor 5 [Lotus japonicus]	862	862	100%	0.0	
ABF50224.1	Nod factor perception protein [Medicago truncatula]	839	839	100%	0.0	
CAO02956.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	740	740	83%	0.0	
CAO02958.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	733	733	82%	0.0	
CAO02933.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02934.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02935.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02938.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02939.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02952.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. longiaculeata] >emb CAO02955.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02957.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02959.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02967.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02971.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02972.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02973.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	725	725	81%	0.0	
CAO02840.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	723	723	81%	0.0	
CAO02951.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	723	723	81%	0.0	
CAO02941.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02970.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	722	722	81%	0.0	
CAO02966.1	LysM-domain containing receptor-like kinase [Medicago truncatula]	718	718	81%	0.0	
BAI79275.1	LysM type receptor kinase [Lotus japonicus] >dbj BAI79285.1 LysM type receptor kinase [Lotus japonicus]	706	706	100%	0.0	
XP_002268472.1	PREDICTED: hypothetical protein [Vitis vinifera] >emb CBI17584.3 unnamed protein product [Vitis vinifera]	643	643	95%	0.0	
XP_002333288.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF29112.1 serine-threonine protein kinase, plant-type, putative [Ricinus communis]	618	618	96%	6e-175	
XP_002319188.1	predicted protein [Populus trichocarpa] >gb EEE90648.1 predicted protein [Populus trichocarpa]	595	595	100%	7e-168	
ADJ19109.1	truncated Nod-factor receptor 5A [Glycine max]	536	536	56%	4e-150	
BAG85147.1	Nod factor receptor protein [Glycine soja]	519	519	54%	4e-145	
BAG85143.1	Nod factor receptor protein [Glycine soja] >dbj BAG85149.1 Nod factor receptor protein [Glycine soja] >dbj BAG85156.1 Nod factor receptor protein [Glycine soja] >dbj BAG85159.1 Nod factor receptor protein [Glycine max] >dbj BAG85160.1 Nod factor receptor protein [Glycine max] >dbj BAG85161.1 Nod factor receptor protein [Glycine max] >dbj BAG85162.1 Nod factor receptor protein [Glycine max] >dbj BAG85165.1 Nod factor receptor protein [Glycine max] >dbj BAG85168.1 Nod factor receptor protein [Glycine max] >dbj BAG85171.1 Nod factor receptor protein [Glycine max] >dbj BAG85174.1 Nod factor receptor protein [Glycine max] >dbj BAG85177.1 Nod factor receptor protein [Glycine max] >dbj BAG85179.1 Nod factor receptor protein [Glycine max] >dbj BAG85180.1 Nod factor receptor protein [Glycine max]	516	516	54%	3e-144	
BAG85152.1	Nod factor receptor protein [Glycine soja]	516	516	54%	5e-144	
BAG85148.1	Nod factor receptor protein [Glycine soja]	515	515	54%	5e-144	
BAG85175.1	Nod factor receptor protein [Glycine max]	514	514	54%	9e-144	
BAG85144.1	Nod factor receptor protein [Glycine soja] >dbj BAG85145.1 Nod factor receptor protein [Glycine soja]	514	514	54%	1e-143	
BAG85170.1	Nod factor receptor protein [Glycine max]	514	514	54%	1e-143	
BAG85167.1	Nod factor receptor protein [Glycine max]	514	514	54%	1e-143	
BAG85164.1	Nod factor receptor protein [Glycine max]	514	514	54%	1e-143	
BAG85159.1	Nod factor receptor protein [Glycine soja]	514	514	54%	1e-143	
BAG85146.1	Nod factor receptor protein [Glycine soja]	514	514	54%	1e-143	

BAG85153.1	Nod factor receptor protein [Glycine soja]	514	514	54%	2e-143	
BAG85158.1	Nod factor receptor protein [Glycine max]	514	514	54%	2e-143	
BAG85172.1	Nod factor receptor protein [Glycine max]	514	514	54%	2e-143	
BAG85142.1	Nod factor receptor protein [Glycine soja]	513	513	54%	2e-143	
BAG85175.1	Nod factor receptor protein [Glycine max]	513	513	54%	3e-143	
BAG85150.1	Nod factor receptor protein [Glycine soja]	512	513	54%	3e-143	
BAG85173.1	Nod factor receptor protein [Glycine max]	513	513	54%	3e-143	
BAG85157.1	Nod factor receptor protein [Glycine soja]	513	513	54%	4e-143	
BAG85175.1	Nod factor receptor protein [Glycine max]	511	511	54%	8e-143	
BAG85155.1	Nod factor receptor protein [Glycine soja]	511	511	54%	1e-142	
BAG85153.1	Nod factor receptor protein [Glycine max]	511	511	54%	2e-142	
BAG85154.1	Nod factor receptor protein [Glycine soja]	509	509	54%	4e-142	
BAG85159.1	Nod factor receptor protein [Glycine max]	507	507	54%	2e-141	
BAG85156.1	Nod factor receptor protein [Glycine max]	501	501	54%	9e-140	
CAQ92936.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	482	482	58%	8e-134	
CAQ92946.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	485	465	56%	7e-129	
CAQ92942.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	482	462	56%	4e-128	
CAQ92950.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	458	458	55%	9e-127	
AAI19139.1	Putative protein kinase [Oryza sativa Japonica Group] >gb ABF94815.1 Protein kinase domain containing protein [Oryza sativa (japonica cultivar-group)] >gb EAZ26175.1 hypothetical protein OsJ_10042 [Oryza sativa Japonica Group]	426	426	93%	5e-117	
XP_002468236.1	hypothetical protein SORBITRAFT_01g042230 [Sorghum bicolor] >gb EER95234.1 hypothetical protein SORBITRAFT_01g042230 [Sorghum bicolor]	426	426	90%	5e-117	
EA178155.1	hypothetical protein OsI_10648 [Oryza sativa Indica Group]	424	424	93%	2e-116	
CAQ92953.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	417	417	52%	3e-114	
CAQ92964.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02968.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	414	414	52%	1e-113	
CAQ92944.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	408	408	51%	1e-111	
CAQ92948.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	404	404	51%	2e-110	
CAQ92962.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	400	400	51%	3e-109	
XP_002517828.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF45192.1 serine-threonine protein kinase, plant-type, putative [Ricinus communis]	356	356	89%	6e-96	
XP_002250079.1	PREDICTED: hypothetical protein [Vitis vinifera]	348	348	89%	1e-93	
CB128350.3	unnamed protein product [Vitis vinifera]	343	343	89%	3e-92	
AA199791.1	SYM10-like protein [Galega orientalis]	336	336	40%	4e-90	
ABR17863.1	unknown [Picea sitchensis]	333	333	77%	3e-89	
CAN99762.1	hypothetical protein [Vitis vinifera]	328	328	89%	1e-87	
XP_001757824.1	predicted protein [Physcomitrella patens subsp. patens] >gb EDQ67338.1 predicted protein [Physcomitrella patens subsp. patens]	309	309	91%	8e-82	
XP_002311653.1	predicted protein [Populus trichocarpa] >gb EEE89020.1 predicted protein [Populus trichocarpa]	308	308	76%	2e-81	
EA178082.1	hypothetical protein OsI_08480 [Oryza sativa Indica Group]	299	299	88%	8e-79	
CAQ92956.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	298	298	40%	2e-78	
BA179275.1	LysM type receptor kinase [Lotus japonicus]	293	293	92%	5e-77	
XP_001780589.1	predicted protein [Physcomitrella patens subsp. patens] >gb EDQ51621.1 predicted protein [Physcomitrella patens subsp. patens]	285	285	90%	1e-74	
XP_002326051.1	predicted protein [Populus trichocarpa] >gb EEE73651.1 predicted protein [Populus trichocarpa]	285	285	86%	1e-74	
XP_002519756.1	kinase, putative [Ricinus communis] >gb EEF52943.1 kinase, putative [Ricinus communis]	284	284	86%	2e-74	
BA179277.1	LysM type receptor kinase [Lotus japonicus] >dbj BA179287.1 LysM type receptor kinase [Lotus japonicus]	283	283	96%	5e-74	
CB17583.3	unnamed protein product [Vitis vinifera]	277	542	93%	3e-72	
XP_002980805.1	hypothetical protein SELMODRAFT_11326 [Selaginella moellendorffii] >gb EFJ08078.1 hypothetical protein SELMODRAFT_11326 [Selaginella moellendorffii]	275	275	89%	2e-71	
XP_002974484.1	hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii] >gb EFJ24716.1 hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii]	273	273	89%	4e-71	
XP_002277332.1	PREDICTED: hypothetical protein [Vitis vinifera]	272	272	89%	8e-71	
XP_002263442.1	PREDICTED: hypothetical protein [Vitis vinifera]	268	268	93%	2e-69	
BA179276.1	LysM type receptor kinase [Lotus japonicus]	268	268	97%	2e-69	
BA179286.1	LysM type receptor kinase [Lotus japonicus]	267	267	97%	3e-69	
XP_002533279.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF29111.1 serine-threonine protein kinase, plant-type, putative [Ricinus communis]	264	264	88%	3e-68	
XP_002533278.1	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis] >gb EEF29110.1 BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]	263	263	91%	4e-68	
XP_002522569.1	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis] >gb EEF39869.1 BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]	262	262	90%	1e-67	
CB148796.3	unnamed protein product [Vitis vinifera]	259	336	85%	9e-67	

XP_002251933.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF52520.1 serine-threonine protein kinase, plant-type, putative [Ricinus communis]	258	258	86%	2e-66	
XP_002263668.1	PREDICTED: hypothetical protein [Vitis vinifera]	256	256	86%	9e-66	
XP_002263180.1	PREDICTED: hypothetical protein [Vitis vinifera]	254	254	90%	2e-65	
XP_002310777.1	predicted protein [Populus trichocarpa] >gb EEE91227.1 predicted protein [Populus trichocarpa]	253	253	86%	6e-65	
ABQ59612.1	LYK4 [Glycine max]	253	253	95%	8e-65	
XP_002327712.1	predicted protein [Populus trichocarpa] >gb EEE75190.1 predicted protein [Populus trichocarpa]	249	249	86%	9e-64	
NP_001958119.1	Os06g0625200 [Oryza sativa Japonica Group] >dbj BAD37734.1 receptor protein kinase-like [Oryza sativa Japonica Group] >dbj BAF20024.1 Os06g0625200 [Oryza sativa Japonica Group] >gb EZA37689.1 hypothetical protein OsJ_22029 [Oryza sativa Japonica Group]	242	242	86%	8e-62	
XP_002397839.1	predicted protein [Populus trichocarpa] >gb EEE94826.1 predicted protein [Populus trichocarpa]	239	239	86%	7e-61	
CA002561.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	238	238	21%	2e-60	
XP_002508540.1	ATP binding protein, putative [Ricinus communis] >gb EEF50927.1 ATP binding protein, putative [Ricinus communis]	236	236	91%	7e-60	
NP_066689.2	CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/ receptor signaling protein/ transmembrane receptor protein kinase [Arabidopsis thaliana] >dbj BAF92788.1 chitin elicitor receptor kinase 1 [Arabidopsis thaliana]	229	229	81%	1e-57	
XP_002360938.1	predicted protein [Populus trichocarpa] >gb EEE84903.1 predicted protein [Populus trichocarpa]	224	224	91%	2e-56	
XP_002263070.1	PREDICTED: hypothetical protein [Vitis vinifera]	224	224	97%	3e-56	
CB168864.3	unnamed protein product [Vitis vinifera]	224	224	97%	4e-56	

Alignments

Select All Get selected sequences Distance tree of results Multiple alignment

>gb|ABQ59609.1| NFR5a [Glycine max]
 gb|ADJ19105.1| Nod-factor receptor 5A [Glycine max]
 gb|ADJ19108.1| Nod-factor receptor 5A [Glycine max]
 Length=598

Score = 1058 bits (2737), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 527/598 (88%), Positives = 560/598 (93%), Gaps = 1/598 (0%)

Query	1	MAVFFVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVVTYISQSPN	59
Sbjct	1	MAVFF L L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVVTYI+QSPN	60
Query	60	FLSLTSSNIFDTSPLSIARASNLQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQ	119
Sbjct	61	FLSLT++SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQ	120
Query	120	GDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLP IGIQVVIPLFCCKPSKNQLDRGIKYL	179
Sbjct	121	GDSFYFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCCKPSKNQLD+ IKYL	180
Query	180	ITHVWQPNDNVSVFVSNKLGASPDILSENNGQNFTAAANLPLVLPVTLPLDQSPSDG	239
Sbjct	181	IT+VW+P DNVS VS+K GASP+DI+SENNGQNFTAA+NLPLVLPVT LP L +SPSDG	240
Query	240	RKHRIGLPVLIIGISLGCTLLVVVSAILLVVCVCLMKSLNRSASSAETADKLLSGVSGYV	299
Sbjct	241	RK I LPVLIIGISLGCTLLV+V A+LLV V CLMK+LNRSASSAETADKLLSGVSGYV	300
Query	300	SKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRKFEDVTEELKILQKVNHG	359
Sbjct	301	SKPTMYET AI+EATMNLSEQCKIGESVYKANIEGKVLAVKRKFEDVTEELKILQKVNHG	360
Query	360	NLVKLMGVSSDNDGNCFFVVEYAENGSL EEWLFAKSCSETSNRSRTSLTWCQRISIAVDVS	419
Sbjct	361	NLVKLMGVSSDNDGNCFFVVEYAENGSL EEWLFAKSCSDTNSRSRTSLTWCQRISMAVDVA	420
Query	420	MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGVVL	479
Sbjct	421	MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL	480
Query	480	IELLTGRKAMTTKENGVEVVMWKDIWKI FDQENREERLRKWMDPKLDNYYPIDYALSLA	539
Sbjct	481	IELLTGRKAMTTKENGVEVVMWKDIWKI FDQENREERLRKWMDPKLESYYPIDYALSLA	540
Query	540	SLAVNCTADKSLSRPTIAEIVLSLSLLTQSPATLERSLTSSGLDVEATQIVTSISAR	597
Sbjct	541	SLAVNCTADKSLSRPTIAEIVLSLSLLTQSPATLERSLTSSGLDVEATQIVTSI+AR	598

>gb|ADJ19106.1| Nod-factor receptor 5A [Glycine max]
 Length=598

GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
 (10 or fewer PubMed links)

Score = 1057 bits (2733), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 526/598 (87%), Positives = 560/598 (93%), Gaps = 1/598 (0%)

Query	1	MAVFFVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVVTYISQSPN	59
Sbjct	1	MAVFF L L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVVTYI+QSPN	60
Sbjct	1	MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVVTYIAQSPN	60

Query	60	FLSLTSSVSNIFDTSPLSIARASNQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQ	119
Sbjct	61	FLSLT++SNIFDTSPLSIARASN+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQ	120
Query	120	GDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIVVPLPFCCKPSKNQLDRGIKYL	179
Sbjct	121	GDSFYFVATT Y+NLTNW AVMDLNP LS LPIGIVV PLFCCKPSKNQLD+ IKYL	180
Query	180	ITHVWQPNNDVSVFVSNKLGASPDILSENNYGNFTAAASNLVPLVLPVTLPLDQSPSDG	239
Sbjct	181	IT+VW+P DNVS VS+K GASP+DI+SENNYGNFTAA+NLVPLIPVT LP L +SPSDG	240
Query	240	RKHRIGLPVITIGISLGCTLLVVVSAILLVVCVCLMKMSLNRSASSAETADKLLSGVSGYV	299
Sbjct	241	RK I LPVITIGISLGCTLLV+V A+LLV V CLMK+LNRSASSAETADKLLSGVSGYV	300
Query	300	SKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHG	359
Sbjct	301	SKPTMYET AI+EATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHG	360
Query	360	NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLF+KSCS+TSNSR SLTWCQRISIAVDVS	419
Sbjct	361	NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLF+KSCS+TSNSR SLTWCQRIS+AVDV+	420
Query	420	MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGVVL	479
Sbjct	421	MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPM KIDVFAFGVVL	480
Query	480	IELLTGRKAMTTKENGVEVVMWLDIWKIFDQEEENREERLRKWMDPKLDNYPIDYALSLA	539
Sbjct	481	IELLTGRKAVTTKENGVEVVMWLDIWKIFDQEEENREERLRKWMDPKLESYPIDYALSLA	540
Query	540	SLAVNCTADKSLSRPTIAEIVLSLSLTPSPATLERSLTSSGLDVEATQIVTSISAR	597
Sbjct	541	SLAVNCTADKSLSRPTIAEIVLSLSLTPSPATLERSLTSSGLDVEATQIVTSI+AR	598

>gb|ADJ19107.1|  Nod-factor receptor 5A [Glycine max]
Length=598

GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
(10 or fewer PubMed links)

Score = 1055 bits (2728), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 525/598 (87%), Positives = 560/598 (93%), Gaps = 1/598 (0%)

Query	1	MAVFFVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVVTYISQSPN	59
Sbjct	1	MAVFF L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVVTYI+QSPN	60
Query	60	FLSLTSSVSNIFDTSPLSIARASNQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQ	119
Sbjct	61	FLSLT++SNIFDTSPLSIARASN+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQ	120
Query	120	GDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIVVPLPFCCKPSKNQLDRGIKYL	179
Sbjct	121	GDSFYFVATT SYENLTNWRVMDLNPVLSPNKLPFIGIVVFPFCCKPSKNQLDKEIKYL	180
Query	180	ITHVWQPNNDVSVFVSNKLGASPDILSENNYGNFTAAASNLVPLVLPVTLPLDQSPSDG	239
Sbjct	181	IT+VW+P DNVS VS+K GASP+DI+SENNYGNFTAA+NLVPLIPVT LP L +SPSDG	240
Query	240	RKHRIGLPVITIGISLGCTLLVVVSAILLVVCVCLMKMSLNRSASSAETADKLLSGVSGYV	299
Sbjct	241	RKGIIRLPVITIGISLGCTLLVVLAVLLVYVYCLMKTLNRSASSAETADKLLSGVSGYV	300
Query	300	SKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHG	359
Sbjct	301	SKPTMYET AI+EATMNLSEQCKIGESVYKANIEGKVLAVKRFK+DVTEELKILQKVNHG	360
Query	360	NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLF+KSCS+TSNSR SLTWCQRISIAVDVS	419
Sbjct	361	NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLF+KSCS+TSNSR SLTWCQRIS+AVDV+	420
Query	420	MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGVVL	479
Sbjct	421	MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPM KIDVFAFGVVL	480
Query	480	IELLTGRKAMTTKENGVEVVMWLDIWKIFDQEEENREERLRKWMDPKLDNYPIDYALSLA	539
Sbjct	481	IELLTGRKA+TTKENGVEVVMWLDIWKIFDQEEENREERL+KWMDPKL++YYPIDYALSLA	540
Query	540	SLAVNCTADKSLSRPTIAEIVLSLSLTPSPATLERSLTSSGLDVEATQIVTSISAR	597
Sbjct	541	SLAVNCTADKSLSRPTIAEIVLSLSLTPSPATLERSLTSSGLDVEATQIVTSI+AR	598

>gb|ADJ19112.1|  Nod-factor receptor 5B [Glycine max]
Length=599

GENE ID: 100498857 NFR5b | Nod-factor receptor 5B [Glycine max]
(10 or fewer PubMed links)

Score = 1029 bits (2661), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 530/599 (88%), Positives = 556/599 (92%), Gaps = 2/599 (0%)

Query	1	MAVFFVSLTLGAQILYVVM-FFTCIEAQSQQTNGTNFSCPSNSPPSC-ETYVVTYISQSP	58
Sbjct	1	MAVFF L L +QIL +VLM FFT I AQSQQTN TNFSCPS+SPP ETYVVTYI+QSP	60
Query	59	NFLSLTSSVSNIFDTSPLSIARASNQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEIN	118
Sbjct	61	NFLSLT+SNIFDTSPLSIARASN+ E+DKLI QVLLIPVTCGCTGNRSFANISYEIN	120
Query	119	QGDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIVVPLPFCCKPSKNQLDRGIKY	178
		GDSFYFVATT Y+NLTNW VMDLNP LS TLPIGIVV PLFCCKPSKNQLD+GIKY	

Sbjct	121	PGDSFYFVATTSYENLTNWRVMDLNPSSLSPNTLPIGIQVVFPLFCKCPSKNQLDKGIKY	180
Query	179	LITHVWQPNNDNVSVSNKLGASPDILSENNYGQNFATAASNLPVLIPVTLPLDIIQSPSD	238
Sbjct	181	LIT+VWQP+DNVS VS K GASP+DILSENNYGQNFATAASNLPVLIPVT LP L QSPSD	240
Sbjct	181	LITYVWQPSDNVSLVSEKFGASPEDILSENNYGQNFATAANNLPVLIPVTRLPVLAQSPSD	240
Query	239	GRKHRIGLPVIIGISLGCTLLVVVSAILLVVCVCLMKMSLNRSASSAETADKLLSGVSGY	298
Sbjct	241	VRKGGIRLPVIIGISLGCTLLVVVLAVLLVYVYCLKIKSLNRSASSAETADKLLSGVSGY	300
Query	299	VSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVN	358
Sbjct	301	VSKPTMYETAI+EATMNLSEQCKIGESVYKANIEGKVLAVKRFKE+VTEELKILQKVN	360
Query	359	GNLVKLMGVSSDNDGNCFFVVEYAENGSLLEEWLFAKSCSETSNRSRTSLTWCQRISIAVDV	418
Sbjct	361	GNLVKLMGVSSDNDGNCFFVVEYA+NGSL+EWLF KSCS+TS+SR SLTWCQRISIAVDV	420
Query	419	SMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGVV	478
Sbjct	421	+MGLQYMHEHAYPRIVHRDI SSNILLDSNFKAKIANFSMARTFTNP M KIDVFAFGVV	480
Query	479	LIELLTGRKAMTTKENGVEVMLWKDIWKIFDQENREERLRKWMMPKLDNYYPIDYALS	538
Sbjct	481	LIELLTGRKAMTTKENGVEVMLWKDIWKIFDQENREERLRKWMMPKLESYYPIDYALS	540
Query	539	ASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATLERSLTSSGLDVEATQIVTSISAR	597
Sbjct	541	ASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATLERSLTSSGLDVEATQIVTSI+AR	599

>gb|ADJ19111.1|  Nod-factor receptor 5B [Glycine max]
Length=599

GENE ID: 100498857 NFR5b | Nod-factor receptor 5B [Glycine max]
(10 or fewer PubMed links)

Score = 1028 bits (2657), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 529/599 (88%), Positives = 555/599 (92%), Gaps = 2/599 (0%)

Query	1	MAVFFVSLTLGAQILYVVLN-FFTCIEAQSQQTNGTNFSCPSNSPPSC-ETYVITYISQSP	58
Sbjct	1	MAVEF L L +QIL +VLM FFT I AQSQQTN TNFSCPS+SPP ETYVITYI+QSP	60
Sbjct	1	MAVFFSLPLRSQILCLVLMLEFFTNIQAQSQQTNETNFSCPSDPPSPSCETYVITYIAQSP	60
Query	59	NFLSLTSVSNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEIN	118
Sbjct	61	NFLSLTS+SNIFDTSPLSIARASNL+ E+DKLI QVLLIPVTCGCTGNRSFANISYEIN	120
Sbjct	61	NFLSLTISI SNIFDTSPLSIARASNLEPEDDKLIADQVLLIPVTCGCTGNRSFANISYEIN	120
Query	119	QGDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVFPLFCKCPSKNQLDRGIKY	178
Sbjct	121	GDSFYFVATT Y+NLTNW VMDLNP LS TLPIGIQVVF PLFCKCPSKNQLD+GIKY	180
Sbjct	121	PGDSFYFVATTSYENLTNWRVMDLNPSSLSPNTLPIGIQVVFPLFCKCPSKNQLDKGIKY	180
Query	179	LITHVWQPNNDNVSVSNKLGASPDILSENNYGQNFATAASNLPVLIPVTLPLDIIQSPSD	238
Sbjct	181	LIT+VWQP+DNVS VS K GASP+DILSENNYGQNFATAASNLPVLIPVT LP L QSPSD	240
Sbjct	181	LITYVWQPSDNVSLVSEKFGASPEDILSENNYGQNFATAANNLPVLIPVTRLPVLAQSPSD	240
Query	239	GRKHRIGLPVIIGISLGCTLLVVVSAILLVVCVCLMKMSLNRSASSAETADKLLSGVSGY	298
Sbjct	241	VRKGGIRLPVIIGISLGCTLLVVVLAVLLVYVYCLKIKSLNRSASSAETADKLLSGVSGY	300
Query	299	VSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVN	358
Sbjct	301	VSKPTMYETAI+EATMNLSEQCKIGESVYKANIEGKVLAVKRFKE+VTEELKILQKVN	360
Sbjct	301	VSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKENVTEELKILQKVN	360
Query	359	GNLVKLMGVSSDNDGNCFFVVEYAENGSLLEEWLFAKSCSETSNRSRTSLTWCQRISIAVDV	418
Sbjct	361	GNLVKLMGVSSDNDGNCFFVVEYA+NGSL+EWLF KSCS+TS+SR SLTWCQRISIAVDV	420
Sbjct	361	GNLVKLMGVSSDNDGNCFFVVEYAQNGSLDEWLFYKSCSDTSDSRASLTWCQRISIAVDV	420
Query	419	SMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGVV	478
Sbjct	421	+MGLQYMHEHAYPRIVHRDI SSNILLDSNFKAKIANFSMARTFTNP M KIDVFAFGVV	480
Sbjct	421	AMGLQYMHEHAYPRIVHRDIASSNILLDSNFKAKIANFSMARTFTNPTMPKIDVFAFGVV	480
Query	479	LIELLTGRKAMTTKENGVEVMLWKDIWKIFDQENREERLRKWMMPKLDNYYPIDYALS	538
Sbjct	481	LIELLTGRKAMTTKENGVEVMLWKDIWKIFDQENREERLRKWMMPKLESYYPIDYALS	540
Sbjct	481	LIELLTGRKAMTTKENGVEVMLWKDIWKIFDQENREERLRKWMMPKLESYYPIDYALS	540
Query	539	ASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATLERSLTSSGLDVEATQIVTSISAR	597
Sbjct	541	ASLAVNCTADKSLSRPTIAEIVLSLSLLTQPS PATLERSLTSSGLDVEATQIVTSI+AR	599
Sbjct	541	ASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSVTLERSLTSSGLDVEATQIVTSIAAR	599

>gb|ABQ59613.1| NFR5b [Glycine max]
Length=515

Score = 909 bits (2348), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 454/504 (90%), Positives = 474/504 (94%), Gaps = 0/504 (0%)

Query	94	QVLLIPVTCGCTGNRSFANISYEINQGDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLP	153
Sbjct	12	QVLLIPVTCGCTGNRSFANISYEIN GDSF FVATT Y+NLTNW VMDLNP LS TLP	71
Sbjct	12	QVLLIPVTCGCTGNRSFANISYEINPGDSFNFVATTSYENLTNWRVMDLNPSSLSPNTLP	71
Query	154	IGIQVVFPLFCKCPSKNQLDRGIKYLITHVWQPNNDNVSVSNKLGASPDILSENNYGQ	213
Sbjct	72	IGIQVVFPLFCKCPSKNQLD+GIKYLIT+VWQP+DNVS VS K GASP+DILSENNYGQ	131
Sbjct	72	IGIQVVFPLFCKCPSKNQLDKGIKYLITYVWQPSDNVSLVSEKFGASPEDILSENNYGQ	131
Query	214	FTAAANLPVLIPVTLPLDIIQSPSDGRKHRIGLPVIIGISLGCTLLVVVSAILLVVCVCL	273
Sbjct	132	FTAAANLPVLIPVT LP L Q PSD RK I LPVIIGISLGCTLLVVV A+LLV V CL	191
Sbjct	132	FTAAANNLPVLIPVTRLPVLAQFSDVRKGGIRLPVIIGISLGCTLLVVVLAVLLVYVYCL	191
Query	274	KMKSLNRSASSAETADKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIE	333
Sbjct	192	K+KSLNRSASSAETADKLLSGVSGYVSKPTMYET AI+EATMNLSE+CKIGESVYKANIE	251
Sbjct	192	KIKSLNRSASSAETADKLLSGVSGYVSKPTMYETDAIMEATMNLSECKIGESVYKANIE	251
Query	334	GKVLAVKRFKEDVTEELKILQKVNHNGLVLMGVSSDNDGNCFFVVEYAENGSLLEEWLFA	393
Sbjct	252	GKVLAVKRFKE+VTEELKILQKVNHNGLVLMGVSSDNDGNCFFVVEYA+NGSL+EWLF	311
Sbjct	252	GKVLAVKRFKENVTEELKILQKVNHNGLVLMGVSSDNDGNCFFVVEYAQNGSLDEWLFY	311


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Query 394 KSCSETSNSRSTSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKI 453
          KSCS+TS+SR SLTWCQRISIAVDV+MGLQYMHEHAYPRIVHRDI SSNILLDSNFKAKI
Sbjct 312 KSCSDTSDSRASLTWCQRISIAVDVAMGLQYMHEHAYPRIVHRDIASSNILLDSNFKAKI 371

Query 454 ANFSMARTFTNPMMSKIDVFAFGVVLLIELLTGRKAMTTKENGEVVMWKDIWKIFDQEEEN 513
          ANFSMARTFTNP M KIDVFAFGVVLLIELLTGRKAMTTKENGEVVMWKDIWKIFDQEEEN
Sbjct 372 ANFSMARTFTNPMPKIDVFAFGVVLLIELLTGRKAMTTKENGEVVMWKDIWKIFDQEEEN 431

Query 514 REERLRKWMMPKLDNYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPAT 573
          REERL+KWMMPKLDNYYPIDYALSLASLAVNCTADKSLSR TIAEIVLSLSLLTQPSPAT
Sbjct 432 REERLRKWMMPKLESYYPIDYALSLASLAVNCTADKSLSRSTIAEIVLSLSLLTQPSPAT 491

Query 574 LERSLTSSGLDVEATQIVTSISAR 597
          LERSLTSSGLDVEATQIVTSI+AR
Sbjct 492 LERSLTSSGLDVEATQIVTSIAAR 515

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>emb|CAE02593.1| SYM10 protein [Pisum sativum]
 emb|CAE02594.1| SYM10 protein [Pisum sativum]
 Length=594

Score = 870 bits (2247), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 437/600 (72%), Positives = 502/600 (83%), Gaps = 9/600 (1%)

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Query 1 MAVFFVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVYISQSPN 59
          MA+FF L + L++ LMFF T I AQ Q +GTNFSQP +SPSCETYVYI ++SPN
Sbjct 1 MAIFF--LPSSSHALFLALMFFVTNISAQPLQLSGTNFSCFVDSPPSCETYVYIFARSPN 58

Query 60 FLSLTSSVSNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQ 119
          FLSLT++S+IFD SPLSIA+ASN++ E+ KL+ QVLLIPVTCGCT NR FAN +Y I
Sbjct 59 FLSLTNISDIFDMSPLSIKASNIEDEDKKLVEGQVLLIPVTCGCTNRNYFANFTYTIKL 118

Query 120 GDSFYFVATTLYQNLTNWHAVMMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYL 179
          GD+++ V+TT YQNLTN+ + + NP LS LP I+VV+PLFCKCPSKNQL +GIK+L
Sbjct 119 GDNYFIVSTTSYQNLTNVEMENFNPNLSPNLLPPEIKVVVPLFCKCPSKNQLSKGKIKHL 178

Query 180 ITHVWQPNNDVSVFVSNKLGASPDILSENNYQNFATAASNLPVLIPVTLPLDILQSPSDG 239
          IT+VWQ NDNV+ VS+K GAS D+ +ENN QNFATA++N+P+LIPVT LP + Q S+G
Sbjct 179 ITYVWQANDNVTRVSSKFGASQVDMFTENN--QNFATASTNVPIIPVTKLPVIDQPPSSNG 236

Query 240 RKHRIGLPV-IIGISLGLTLLVVVSAILLVCCCLMKKSLNRSASSAETADKLLSGVSGY 298
          RK+ P IIGISLGC VVV + LV V CLKMK LNRS S AETADKLLSGVSGY
Sbjct 237 RKNSTQKPAFIIGISLGCFAFFVVVLTLSLVVYVCLMKRLNRSTSLAETADKLLSGVSGY 296

Query 299 VSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNH 358
          VSKPTMYE AI+EATMNLSE CKIGESVYKANI+G+VLAVK+ K+D +EELKILQKVNH
Sbjct 297 VSKPTMYEMDAIMEATMNLSENCKIGESVYKANIDGRVLAVKKIKKDASEELKILQKVNH 356

Query 359 GNLVKLMGVSSDNDGNCFFVVEYAENGSLLEWLFKASCSETSNSRSTSLTWCQRISIAVDV 418
          GNLVKLMGVSSDNDGNCFF+VVEYAENGSL+EWLF++S S+TSNS SLTW QRI++AVDV
Sbjct 357 GNLVKLMGVSSDNDGNCFLVVEYAENGSLDEWLFSES-SKTSNSVVSLSLTSQRTITVAVDV 415

Query 419 SMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGVV 478
          ++GLQYMHEH YPRI+HRDIT+SNILLDSNFKAKIANFSMART TN MM KIDVFAFGVV
Sbjct 416 AVGLQYMHEHTYPRIIHRDITTSNILLDSNFKAKIANFSMARTSTNSMMPKIDVFAFGVV 475

Query 479 LIELLTGRKAMTTKENGEVVMWKDIWKIFDQEEENREERLRKWMMPKLDNYYPIDYALSL 538
          LIELLTG+KA+TT ENGEVV+LWKD WKIFD E NREE LRKWMMPKL+N+YPID ALSL
Sbjct 476 LIELLTGKKAITTMENGEVVILWKDFWKIFDLEGNREESLRKWMMPKLENFYPIDNALSL 535

Query 539 ASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPA-TLERSLTSSGLDVEATQIVTSISAR 597
          ASLAVNCTADKSLSRP+IAEIVL LSL Q S LERSLT SGLDVEAT +VTSI AR
Sbjct 536 ASLAVNCTADKSLSRPSIAEIVLCLSLNQSSEPMLESLT-SGLDVEATHVVTISIVAR 594

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>gb|ADJ19110.1| truncated Nod-factor receptor 5A [Glycine max]
 Length=501

GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
 (10 or fewer PubMed links)

Score = 866 bits (2238), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 434/501 (86%), Positives = 463/501 (92%), Gaps = 1/501 (0%)

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Query 1 MAVFFVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVYISQSPN 59
          MAVFF L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPSCETYVYI+QSPN
Sbjct 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVYIAQSPN 60

Query 60 FLSLTSSVSNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQ 119
          FLSLT++SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQ
Sbjct 61 FLSLTNISNIFDTSPLSIARASNLPEMDKLVDQVLLVPVTCGCTGNRSFANISYEINQ 120

Query 120 GDSFYFVATTLYQNLTNWHAVMMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYL 179
          GDSFYFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYL
Sbjct 121 GDSFYFVATTSYENLTNWRVMDLNPVLSPNKLPPIGIQVVFPLFCKCPSKNQLDKEIKYL 180

Query 180 ITHVWQPNNDVSVFVSNKLGASPDILSENNYQNFATAASNLPVLIPVTLPLDILQSPSDG 239
          IT+VW+P DNVS VS+K GASP+DI+SENNYQNFATA+NLVLPVLPVT LP L +SPSDG
Sbjct 181 ITYVWKPQDNVSVLSVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDG 240

Query 240 RKHRIGLPV-IIGISLGLTLLVVVSAILLVCCCLMKKSLNRSASSAETADKLLSGVSGYV 299
          RK I LPVFIIGISLGLTLLV+V A+LLV V CLKMK+LNRSASSAETADKLLSGVSGYV
Sbjct 241 RKGIRLPVFIIGISLGLTLLVLVLAVLVVYVCLMKMTLNRSASSAETADKLLSGVSGYV 300

Query 300 SKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHG 359
          SKPTMYET AI+EATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHG
Sbjct 301 SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHG 360

Query 360 NLVKLMGVSSDNDGNCFFVVEYAENGSLLEWLFKASCSETSNSRSTSLTWCQRISIAVDV 419
          NLVKLMGVSSDNDGNCFFVVEYAENGSL+EWLF+KSCS+TSNSR SLTWCQRIS+AVDV+
Sbjct 361 NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFKSCSDTSNSRASLTWCQRISMAVDVA 420

Query 420 MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGVV 479
          MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMM KIDVFAFGVV
Sbjct 421 MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMPKIDVFAFGVV 480

Query 480 IELLTGRKAMTTKENGEVVM 500



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Sbjct 481 IELLTGRKAMTTKENGVEVVML 501
IELLTGRKAMTTKENGVEVVML

>emb|CAE02595.1| SYM10 protein [Pisum sativum]
emb|CAE02596.1| SYM10 protein [Pisum sativum]
gb|ADB45277.1| Nod factor recognition protein [Pisum sativum]
Length=594

Score = 865 bits (2236), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 435/600 (72%), Positives = 501/600 (83%), Gaps = 9/600 (1%)

Query	1	MAVFFVSLTLGAQILYVVMFF--TCIEAQSQQTNGTNFSCPSNSPPSCETYVVTYISQSPN	59
Sbjct	1	MA+FF L + L++ LMFF T I AQ Q +GTNFSCP +SPPSCETYVTY ++SPN	58
		MAIFF--LPSSSHALFLALMFFVTNISAQPLQLSGTNFSCPVDSPSCETYVTYFARSPN	
Query	60	FLSLTSVSNIFDTSPLSIARASNLOHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQ	119
Sbjct	59	FLSLT++S+IFD SPLSIA+ASN++ E+ KL+ GQVLLIPVTCGCT NR FAN +Y I	118
		FLSLTNTSDFIDMSPLSIARASNIEDEDKKLVEGQVLLIPVTCGCTRNRYFANFTYTIKL	
Query	120	GDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPFIGIQVVIPLFCCKCPSKNQLDRGIKYL	179
Sbjct	119	GD+++ V+TT YQNLTN+ + + NP LS LP I+VV+PLFCCKCPSKNQL +GIK+L	178
		GDNYFIIVSTTSYQNLTNYVEMENFNPNLSPNLLPPEIKVVVPLFCCKCPSKNQLSKGIKHL	
Query	180	ITHVWQPNNDVSVFSNKLGAQPDI SENNYGQNFTAASNLPVLIPVTLPLDIQSPSDG	239
Sbjct	179	IT+VWQ NDNV+ VS+K GAS D+ +ENN QNFTA++N+P+LIPVT LP + Q S+G	236
		ITYVWQANDNVTRVSSKFGASQVDMFTENN--QNFTASTNPILIPVTKLPVIDQPSSNG	
Query	240	RKHRIGLPV--IIGISLGLTLLVVVSAILLVVCVCLMKSLNRSASSAETADKLLSGVSGY	298
Sbjct	237	RK+ P IIGISLGC VVV + LV V CLKMK LNRS S AETADKLLSGVSGY	296
		RKNSTQKPAFIIGISLGCFFVVVLTLSLVYVYCLMKRLNRSTSLAETADKLLSGVSGY	
Query	299	VSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNH	358
Sbjct	297	VSKPTMYE AI+EATMNLSE CKIGESVYKANI+G+VLAVK+ K+D +EELKILQKVNH	356
		VSKEPTMYEMDAIMEATMNLSENCKIGESVYKANIDGRVLAVKKIKKDAEELKILQKVNH	
Query	359	GNLVKLMGVSSDNDGNCFFVVEYAENGSLLEEWLFAKSCSETSNSRSTSLTWCQRISIAVDV	418
Sbjct	357	GNLVKLMGVSSDN+GNCF+VVEYAENGSL+EWLF++ S+TSNS SLTW QRI++AVDV	415
		GNLVKLMGVSSDNEGNCFLVVEYAENGSLDEWLFSE-LSKTSNSVSLTWSQRITVAVDV	
Query	419	SMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGVV	478
Sbjct	416	++GLQYMHEH YPRI+HRDIT+SNILLDSNFKAKIANFSMART TN MM KIDVFAFGVV	475
		AVGLQYMHEHTYPRIIHRDITTSNILLDSNFKAKIANFSMARTSTNMPMKIDVFAFGVV	
Query	479	LIELLTGRKAMTTKENGVEVVMLWKDIWKIFDQENREERLRKWMDPKLDNYYPIDYALSL	538
Sbjct	476	LIELLTG+KA+TT ENGEVV+LWKD WKIFD E NREE LRKWMDPKL+N+YPID ALSL	535
		LIELLTGKKAITTMENGVEVILWKDFWKIFDLEGNREESLRKWMDPKLENFYPIDNALS	
Query	539	ASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSA-TLERSLTSSGLDVEATQIVTTSISAR	597
Sbjct	536	ASLAVNCTADKSLSRP+IAEIVL LSLL Q S LERSLT SGLDVEAT +VTSI AR	594
		ASLAVNCTADKSLSRPSIAEIVLCLSLNQSSSEPMIERSLT-SGLDVEATHVVTISIVAR	

>emb|CAE02597.1|  Nod-factor receptor 5 [Lotus japonicus]
emb|CAE02598.1|  Nod-factor receptor 5 [Lotus japonicus]
Length=595

GENE ID: 100034751 NFR5 | Nod-factor receptor 5 [Lotus japonicus]
(10 or fewer PubMed links)

Score = 862 bits (2227), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 432/601 (71%), Positives = 502/601 (83%), Gaps = 10/601 (1%)

Query	1	MAVFFVSLTLGAQILYVVMFFTC-IEAQSQQTNGTNFSCPSNSPPSCETYVVTYISQSPN	59
Sbjct	1	MAVEF LT G+ L++ L I A+S++ +G +FSCP +SPPSCETYVTY +QSPN	58
		MAVEF--LTSGSLFLALTLFTNIAARSEKISGPDFSCFPVDSPPSCETYVTYTAQSPN	
Query	60	FLSLTSVSNIFDTSPLSIARASNLOHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQ	119
Sbjct	59	LSLT++S+IFD SPLSIARASN+ +DKL+PGQVLL+PVTGCG GN S AN SY+I	118
		LLSLTNTSDFIDISPLSIARASNIDAGKDKLVPGQVLLVPVTCGACAGNHSSANTSYYIQL	
Query	120	GDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPFIGIQVVIPLFCCKCPSKNQLDRGIKYL	179
Sbjct	119	GDS+ FVATTLY+NLTNW+ V NPG++ + LP ++VV PLFC+CPCKNQL++GI+YL	178
		GDSYDFVATTLYENLTNWNIVQASNPQVNPYLLPERVKVVFPLFCRCPSKNQLNKGIOYL	
Query	180	ITHVWQPNNDVSVFSNKLGAQPDI SENNYGQNFTAASNLPVLIPVTLPLDIQSPSDG	239
Sbjct	179	IT+VW+PNDNVS VS K GASP DIL+EN YGQ+FTAA+NLP+LIPVT LP+L Q S+G	238
		ITYVWKPNDNVSLVSAKFGASPADILTENRYGQDFTAATNLPIIPVTLPELTQPSSNG	
Query	240	RKHRIGLPVVIIGISLGLTLLVVVSAILLVVCVCLMKSLNRSASSAETADKLLSGVSGYV	299
Sbjct	239	RK I L VI+GI+LGCTLL V LV V C + K+LNR+ASSAETADKLLSGVSGYV	298
		RKSSIHLLVLIGITLGLTLLTAVLTGTLVYVYCRKKALNRTASSAETADKLLSGVSGYV	
Query	300	SKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKE-DVTEELKILQKVNH	358
Sbjct	299	SKP +YE I+EAT+ S++CK+GESVYKANIEG+V+AVK+ KE EELKILQKVNH	358
		SKPNVYIIDLIMEATKDFSDCKVGEVYKANIEGRVAVVAVKKIEGGANEELKILQKVNH	
Query	359	GNLVKLMGVSSDNDGNCFFVVEYAENGSLLEEWLFAKSCSETSNSRSTSLTWCQRISIAVDV	418
Sbjct	359	GNLVKLMGVSS DGNCF+VVEYAENGSL EWL+KS S + SLTW QRISIAVDV	414
		GNLVKLMGVSSSGYDGNCFVVEYAENGSLAEWLFSKS----SGTPNSLTWSQRISIAVDV	
Query	419	SMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGVV	478
Sbjct	415	++GLQYMHEH YPRI+HRDIT+SNILLDSNFKAKIANF+MART TNMM KIDVFAFGV+	474
		AVGLQYMHEHTYPRIIHRDITTSNILLDSNFKAKIANFAMARTSTNMPMKIDVFAFGVL	
Query	479	LIELLTGRKAMTTKENGVEVVMLWKDIWKIFDQENREERLRKWMDPKLDNYYPIDYALSL	538
Sbjct	475	LIELLTGRKAMTTKENGVEVVMLWKD+W+IFD EENREER+RKWMDP L++Y ID ALSL	534
		LIELLTGRKAMTTKENGVEVVMLWKDMWEIFDIEENREERIRKWMDPNLESFYHIDNALS	
Query	539	ASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSA-ATLERSLTSSGLDVE-ATQIVTTSISA	596
Sbjct	535	ASLAVNCTADKSLSRP++AEIVLSLS LTQ S TLERSLTSSGLDVE IVTSI+A	594
		ASLAVNCTADKSLSRPSMAEIVLSLSFLTQSSNPTLERSLTSSGLDVEDDAHIVTTSITA	
Query	597	R 597	
Sbjct	595	R 595	

>gb|ABF50224.1| Nod factor perception protein [Medicago truncatula]
Length=595

Score = 839 bits (2168), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 422/599 (70%), Positives = 493/599 (82%), Gaps = 6/599 (1%)

Query	1	MAVFFVSLTLGAQILYVVLMEFTTCIEAQSQQTNGTNFSCPSNSPPSCETYVYTIYSQSPNF	60
		M+ FF+ + A L ++L F T I AQ + TNF+CP +SPSCETYV Y +QSPNF	
Sbjct	1	MSAFFLPSSSHALFLVLMFLTNISAQPLYISETNFTCPVDSPPSCETYVAYRAQSPNF	60
Query	61	LSLTSVSNIFDTSPLSIARASNQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQG	120
		LSL+++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTCGCT N SFANI+Y I QG	
Sbjct	61	LSLSNISDIFNLSPLRIAKASNIEAEDKKLIPDQLLLVPVTCGCTKNHSFANITYSIKQG	120
Query	121	DSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYL	180
		D+F+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCKCPSKNQL++GIKYL	
Sbjct	121	DNFFILSITSYQNLTNYLEFKNFNPNSPTLLPLDTPKVSVPFLFCKCPSKNQLNKGIKYL	180
Query	181	THVWQPNNDVSVFVSNKLGASPDILSENNGYQNFNTAASNLPVLIPTVLLPDLIQSPSDGR	240
		T+VWQ NDNV+ VS+K GAS ++L+ENN+ NFTA++N VLIPTV LP L Q S+GR	
Sbjct	181	TYVWQDNNDVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPTVSLPKLDQSSNGR	238
Query	241	KHRI-GLPVIIGISLGTLLVVSAILVVCVCLMKSLNRSASSAETADKLLSGVSGYV	299
		K L +IIGISLG ++V + LV V CLKMK LNRS SS+ETADKLLSGVSGYV	
Sbjct	239	KSSSQNLALIIGISLGAFFILVLTLSLVYVYCLMKRLNRSTSSSETADKLLSGVSGYV	298
Query	300	SKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHG	359
		SKPTMYE AI+E T NLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELKILQKVNHG	
Sbjct	299	SKPTMYEIDAIMEGTTNLSNCKIGESVYKANIDGRVLAVKKIKKDAEELKILQKVNHG	358
Query	360	NLVKLMGVSSDNDGNCFFVVEYAENGSLLEEWLFAKSCSETSNRSTSLTWCQRISIAVDVS	419
		NLVKLMGVSSDNDGNCFFVVEYAENGSLLEEWLF++S S+TSNS SLTW QRI+IA+DV+	
Sbjct	359	NLVKLMGVSSDNDGNCFLVVEYAENGSLLEEWLFSES-SKTSNSVVSILTWSQRITIAMDVA	417
Query	420	MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGVVL	479
		+GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART TN MM KIDVFAFGVVL	
Sbjct	418	IGLQYMHEHTYPRIIHRDITSSNILLGSNFKAKIANFGMARTSTNSMMPKIDVFAFGVVL	477
Query	480	IELLTGRKAMTTKENGVEVVLWKDIWKIFDQENREERLRKWMDPKLDNYYPIDYALSLA	539
		IELLTG+KAMTTKENGVEVV+LWKD WKIFD E NREERLRKWMDPKL+++YPID ALSLA	
Sbjct	478	IELLTGKAMTTKENGVEVVLWKDFWKIFDLEGNREERLRKWMDPKLESFYPIDNALSLA	537
Query	540	SLAVNCTADKSLSRPTIAEIVLSLSLTPQSPA-TLERSLTSSGLDVEATQIVTSISAR	597
		SLAVNCTADKSLSRPTIAEIVL LSL QPS LERSLT SGLD EAT +VTS+ AR	
Sbjct	538	SLAVNCTADKSLSRPTIAEIVLCLSLLNQPSSEPMLESLT-SGLDAEATHVVTSVIAR	595

>emb|CA002956.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
Length=498

Score = 740 bits (1910), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 358/497 (72%), Positives = 420/497 (84%), Gaps = 4/497 (0%)

Query	45	PSCETYVYTIYSQSPNFLSLTSVSNIFDTSPLSIARASNQHEEDKLIPGQVLLIPVTCGC	104
		PSCETYV Y+QSPNFLSL+++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTCGC	
Sbjct	4	PSCETYVAYRAQSPNFLSLSNISDIFNLSPLRIAKASNIEAEDKKLIPDQLLLVPVTCGC	63
Query	105	TGNRSFANISYEINQGDSEFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFC	164
		T N SFANI+Y I QGD+F+ ++ T YQNLTN+ + NP LS LP+ +V +PLFC	
Sbjct	64	TKNHSFANITPYSIKQGDNFFILSITSYQNLTNYLEFKNFNPNSPTLLPLDTPKVSVPFLFC	123
Query	165	KCPSKNQLDRGIKYLITHVWQPNNDVSVFVSNKLGASPDILSENNGYQNFNTAASNLPVLI	224
		KCPSKNQL++GIKYLIT+VWQ NDNV+ VS+K GAS ++L+ENN+ NFTA++N VLI	
Sbjct	124	KCPSKNQLNKGIKYLITYVWQDNNDVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLI	181
Query	225	PVTLPLDLPQSPDGRKHRI-GLPVIIGISLGTLLVVSAILVVCVCLMKSLNRSAS	283
		PVT LP L Q S+GRK L +IIGISLG ++V + LV V CLKMK LNRS S	
Sbjct	182	PVTSPLKLDQSSNGRKSSSQNLALIIGISLGAFFILVLTLSLVYVYCLMKRLNRSTS	241
Query	284	SAETADKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFK	343
		S+ETADKLLSGVSGYVSKPTMYE AI+E TMNLS+ CKIGESVYKANI+G+VLAVK+ K	
Sbjct	242	SSETADKLLSGVSGYVSKPTMYEIDAIMEGTMNLSNCKIGESVYKANIDGRVLAVKKIK	301
Query	344	EDVTEELKILQKVNHNGLVLMGVSSDNDGNCFFVVEYAENGSLLEEWLFAKSCSETSNR	403
		+D +EELKILQKVNHNGLVLMGVSSDNDGNCFFVVEYAENGSLLEEWLF++S S+TSNS	
Sbjct	302	KDASEELKILQKVNHNGLVLMGVSSDNDGNCFLVVEYAENGSLLEEWLFSES-SKTSNSV	360
Query	404	SLTWQQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFT	463
		SLTW QRI+IA+DV++GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART T	
Sbjct	361	VSLTWSQRITIAMDVAIGLQYMHEHTYPRIIHRDITSSNILLGSNFKAKIANFGMARTST	420
Query	464	NPMMSKIDVFAFGVVLIELLTGRKAMTTKENGVEVVLWKDIWKIFDQENREERLRKWM	523
		N MM KIDVFAFGVVLIELLTG+KAMTTKENGVEVV+LWKD WKIFD E NREERLRKWM	
Sbjct	421	NSMMPKIDVFAFGVVLIELLTGKAMTTKENGVEVVLWKDFWKIFDLEGNREERLRKWM	480
Query	524	PKLDNYYPIDYALSLAS	540
		PKL+++YPID ALS+AS	
Sbjct	481	PKLESFYPIDNALSMAS	497

>emb|CA002958.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
Length=492

Score = 733 bits (1892), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 355/494 (71%), Positives = 417/494 (84%), Gaps = 4/494 (0%)

Query	48	ETYVYTIYSQSPNFLSLTSVSNIFDTSPLSIARASNQHEEDKLIPGQVLLIPVTCGCTGN	107
		ETYV Y+QSPNFLSL+++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTCGCT N	
Sbjct	1	ETYVAYRAQSPNFLSLSNISDIFNLSPLRIAKASNIEAEDKKLIPDQLLLVPVTCGCTKN	60
Query	108	RSFANISYEINQGDSEFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCP	167
		SFANI+Y I QGD+F+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCKCP	
Sbjct	61	HSFANITYSIKQGDNFFILSITSYQNLTNYLEFKNFNPNSPTLLPLDTPKVSVPFLFCKCP	120
Query	168	SKNQLDRGIKYLITHVWQPNNDVSVFVSNKLGASPDILSENNGYQNFNTAASNLPVLIPTV	227

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Sbjct 121 SKNQL++GIKYLIT+VWQ NDNV+ VS+K GAS ++L+ENN+ NFTA++N VLIPVT
SKNQLNKGIKYLITYVWQDNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPVT 178

Query 228 LLPDLIQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLVCVCCLKMKSLNRSASSAE 286
LP L Q S+GRK L +IIGISLG ++V + LV V CLKMK LNRS SS+E

Sbjct 179 SLPKLDQPSNNGRKSQQNLALIIGISLGSAFFILVLTLSLVVYVCLMKRLNRSTSSSE 238

Query 287 TADKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDV 346
TADKLLSGVSGYVSKPTMYE AI+E TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D

Sbjct 239 TADKLLSGVSGYVSKPTMYEIDAIMEGTMNLSNCKIGESVYKANIDGRVLAVKKIKKDA 298

Query 347 TEELKILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSLLEWLFASKSETSNSRTSL 406
+EELKILQKVNHNGLVKLMGVSSDNDGNCFF+VVEYAENGSLLEWLF++S S+TSNS SL

Sbjct 299 SEELKILQKVNHNGLVKLMGVSSDNDGNCFLVVEYAENGSLLEWLFSES-SKTSNSVSVSL 357

Query 407 TWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLSDNFKAKIANFSMARTFTNPM 466
TW QRI+IA+DV++GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART TN M

Sbjct 358 TWSQRIPIAMDVAIGLQYMHEHTYPRIIHRDITTSNILLGSNFKAKIANFGMARTSTNSM 417

Query 467 MSKIDVFAFGVVLIELLTGKAMTTKENGVEVVLWKDIWKIFDQEEENREERLRKWMDPKL 526
M KIDVFAFGVVLIELLTG+KAMTTKENGVEV+LWKD WKIFD E NREERLRKWMDPKL

Sbjct 418 MPKIDVFAFGVVLIELLTGKAMTTKENGVEVVLWKDFWKIFDLEGNREERLRKWMDPKL 477

Query 527 DNYYPIDYALSLAS 540
+++YPID ALS+AS

Sbjct 478 ESFPIDNALSMA 491

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>emb|CA002933.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002934.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002935.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
10 more sequence titles

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emb|CA002938.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002939.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002952.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. longiaculeata]
emb|CA002955.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002957.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002959.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002967.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002971.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002972.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002973.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
Length=487

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Score = 725 bits (1871), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 351/489 (71%), Positives = 413/489 (84%), Gaps = 4/489 (0%)

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Query 53 YISQSPNFLSLTSSVSNIFDTSPLSIARASNQHEEDKLIPGQVLLIPVTCGCTGNRSFAN 112
Y +QSPNFLSL++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTGCT N SFAN

Sbjct 1 YRAQSPNFLSLSNISDIFNLSPLRIAKASNIEAEDKKLIPDQLLLVPVTCGCTKNHSFAN 60

Query 113 ISYBINQGDSEFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIGQVVIPLFCKCPSKNQL 172
I+Y I QGD+E+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCKCPSKNQL

Sbjct 61 ITYSIKQGDNFFILSITSYQNLTNYLEFKNFNPNLSPTLLPLDTKVSVPLFCKCPSKNQL 120

Query 173 DRGKYKYLITHVWQPDNDNVSVSNKLGASPDIDISENNYQGNFTAASNLPVLIPVTLTLPDL 232
++GIKYLIT+VWQ NDNV+ VS+K GAS ++L+ENN+ NFTA++N VLIPVT LP L

Sbjct 121 NKGIKYLITYVWQDNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPVTSLPKL 178

Query 233 IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLVCVCCLKMKSLNRSASSAETADKL 291
Q S+GRK L +IIGISLG ++V + LV V CLKMK LNRS SS+ETADKL

Sbjct 179 DQPSNNGRKSQQNLALIIGISLGSAFFILVLTLSLVVYVCLMKRLNRSTSSSETADKL 238

Query 292 LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
LSGVSGYVSKPTMYE AI+E TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK

Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTMNLSNCKIGESVYKANIDGRVLAVKKIKKDAEELK 298

Query 352 ILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSLLEWLFASKSETSNSRTSLTWCQR 411
ILQKVNHNGLVKLMGVSSDNDGNCFF+VVEYAENGSLLEWLF++S S+TSNS SLTW QR

Sbjct 299 ILQKVNHNGLVKLMGVSSDNDGNCFLVVEYAENGSLLEWLFSES-SKTSNSVSVSLTWSQR 357

Query 412 ISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLSDNFKAKIANFSMARTFTNPMMSKID 471
I+IA+DV++GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART TN MM KID

Sbjct 358 ITIAMDVAIGLQYMHEHTYPRIIHRDITTSNILLGSNFKAKIANFGMARTSTNSMMPKID 417

Query 472 VFAGGVVLIELLTGKAMTTKENGVEVVLWKDIWKIFDQEEENREERLRKWMDPKLDNYYP 531
VFAGGVVLIELLTG+KAMTTKENGVEV+LWKD WKIFD E NREERLRKWMDPKL+++YP

Sbjct 418 VFAGGVVLIELLTGKAMTTKENGVEVVLWKDFWKIFDLEGNREERLRKWMDPKLESFYP 477

Query 532 IDYALSLAS 540
ID ALS+AS

Sbjct 478 IDNALSMA 486

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>emb|CA002940.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
Length=487

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Score = 723 bits (1866), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 351/489 (71%), Positives = 412/489 (84%), Gaps = 4/489 (0%)

```

Query 53 YISQSPNFLSLTSSVSNIFDTSPLSIARASNQHEEDKLIPGQVLLIPVTCGCTGNRSFAN 112
Y +QSPNFLSL++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTGCT N SFAN

Sbjct 1 YRAQSPNFLSLSNISDIFNLSPLRIAKASNIEAEDKKLIPDQLLLVPVTCGCTKNHSFAN 60

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Query 113 ISYEINQGDSEFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQL 172
I+Y I QGD+F+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCKCPSKNQL
Sbjct 61 ITYSIKQGDNFFILSITSYQNLNTNLEFKNFNPNSPTLLPLDTKVSVPFLFCKCPSKNQL 120

Query 173 DRGKYLITHVWQPNQDNVSVFVSNKLGASPDILSENNYQGNFTAASNLPVLIPVTLPLPDL 232
++GKIKYLIT+VWQ NDNV+ VS+K GAS ++L+ENN+ NFTA++N VLIPVT LP L
Sbjct 121 NKGIKYLITYVWQNDNNTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPTVTSLPKL 178

Query 233 IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLVCVCCCLKMKS LNRSASSAETADKL 291
Q S+GRK L +IIGISLG ++V + LV V CLKMK LNRS SS+ETADKL
Sbjct 179 DQPSNNGRKSSSNLALIIIGISLGS AFFILVLTLSLVYVYCLKMKRLNRSTSSSETADKL 238

Query 292 LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
LSGVSGYVSKPTMYE AI+E TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK 298

Query 352 ILQKVNHGNIIVKLMGVSSDNDGNCFFVVEYAENGSLLEEWLFAKSCSETSNRSTSLTWCQR 411
ILQKVNHGNIIVKLMGVSSDNDGNCFFVVEYAENGSLLEEWLF++S +TSNS SLTW QR
Sbjct 299 ILQKVNHGNIIVKLMGVSSDNDGNCFLVVEYAENGSLLEEWLFSES-KTSNSVSVSLTWSQR 357

Query 412 ISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKID 471
I+IA+DV++GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART TN MM KID
Sbjct 358 ITIAMDVAIIGLQYMHEHTYPRIIHRDITTSNILLGSNFKAKIANFGMARTSTNSMMPKID 417

Query 472 VFAPGVVLIELLTGKAMTTKENGGEVVLWKDIWKIFDQENREERLRKWMDPKLDNYYP 531
VFAPGVVLIELLTG+KAMTTKENGGEV+LWKD WKIFD E NREERLRKWMDPKL+++YP
Sbjct 418 VFAPGVVLIELLTGKAMTTKENGGEVVLWKDFWKIFDLEGNREERLRKWMDPKLESFYP 477

Query 532 IDYALSLAS 540
ID ALSLAS
Sbjct 478 IDNALSAS 486

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>**emb|CA002951.1** | LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=487

Score = 723 bits (1866), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 351/489 (71%), Positives = 412/489 (84%), Gaps = 4/489 (0%)

```

Query 53 YISQSPNFLSLTSSVSNIFDTSPLSIARASNQHEEDKLIPGQVLLIPVTCGCTGNRSFAN 112
Y +QSPNFLSL+++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTGCT N SFAN
Sbjct 1 YRAQSPNFLSLSNISDIFNLSPRIAKASNIEAEDKKLIPDQLLLPVTCGCTKNHSFAN 60

Query 113 ISYEINQGDSEFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQL 172
I+Y I QGD+F+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCKCPSKNQL
Sbjct 61 ITYSIKQGDNFFILSITSYQNLNTNLEFKNFNPNSPTLLPLDTKVSVPFLFCKCPSKNQL 120

Query 173 DRGKYLITHVWQPNQDNVSVFVSNKLGASPDILSENNYQGNFTAASNLPVLIPVTLPLPDL 232
++GKIKYLIT+VWQ NDNV+ VS+K GAS ++L+ENN+ NFTA++N VLIPVT LP L
Sbjct 121 NKGIKYLITYVWQNDNNTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPTVTSLPKL 178

Query 233 IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLVCVCCCLKMKS LNRSASSAETADKL 291
Q S+GRK L +IIGISLG ++V + LV V CLKMK LNRS SS+ETADKL
Sbjct 179 DQPSNNGRKSSSNLALIIIGISLGS AFFILVLTLSLVYVYCLKMKRLNRSTSSSETADKL 238

Query 292 LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
LSGVSGYVSKPTMYE AI+E T NLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK 298

Query 352 ILQKVNHGNIIVKLMGVSSDNDGNCFFVVEYAENGSLLEEWLFAKSCSETSNRSTSLTWCQR 411
ILQKVNHGNIIVKLMGVSSDNDGNCFFVVEYAENGSLLEEWLF++S S+TSNS SLTW QR
Sbjct 299 ILQKVNHGNIIVKLMGVSSDNDGNCFLVVEYAENGSLLEEWLFSES-SKTSNSVSVSLTWSQR 357

Query 412 ISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKID 471
I+IA+DV++GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART TN MM KID
Sbjct 358 ITIAMDVAIIGLQYMHEHTYPRIIHRDITTSNILLGSNFKAKIANFGMARTSTNSMMPKID 417

Query 472 VFAPGVVLIELLTGKAMTTKENGGEVVLWKDIWKIFDQENREERLRKWMDPKLDNYYP 531
VFAPGVVLIELLTG+KAMTTKENGGEV+LWKD WKIFD E NREERLRKWMDPKL+++YP
Sbjct 418 VFAPGVVLIELLTGKAMTTKENGGEVVLWKDFWKIFDLEGNREERLRKWMDPKLESFYP 477

Query 532 IDYALSLAS 540
ID ALSLAS
Sbjct 478 IDNALSAS 486

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>**emb|CA002941.1** | LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
>**emb|CA002970.1** | LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=487

Score = 722 bits (1863), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 350/489 (71%), Positives = 412/489 (84%), Gaps = 4/489 (0%)

```

Query 53 YISQSPNFLSLTSSVSNIFDTSPLSIARASNQHEEDKLIPGQVLLIPVTCGCTGNRSFAN 112
Y +QSPNFLSL+++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTGCT N SFAN
Sbjct 1 YRAQSPNFLSLSNISDIFNLSPRIAKASNIEAEDKKLIPDQLLLPVTCGCTKNHSFAN 60

Query 113 ISYEINQGDSEFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQL 172
I+Y I QGD+F+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCKCPSKNQL
Sbjct 61 ITYSIKQGDNFFILSITSYQNLNTNLEFKNFNPNSPTLLPLDTKVSVPFLFCKCPSKNQL 120

Query 173 DRGKYLITHVWQPNQDNVSVFVSNKLGASPDILSENNYQGNFTAASNLPVLIPVTLPLPDL 232
++GKIKYLIT+VWQ NDNV+ VS+K GAS ++L+ENN+ NFTA++N VLIPVT LP L
Sbjct 121 NKGIKYLITYVWQNDNNTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPTVTSLPKL 178

Query 233 IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLVCVCCCLKMKS LNRSASSAETADKL 291
Q S+GRK L +IIGISLG ++V + LV V CLKMK LNRS SS+ETADKL
Sbjct 179 DQPSNNGRKSSSNLALIIIGISLGS AFFILVLTLSLVYVYCLKMKRLNRSTSSSETADKL 238

Query 292 LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
LSGVSGYVSKPTMYE AI+E T NLS+ CKIGESVYKAN++G+VLAVK+ K+D +EELK
Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANMDGRVLAVKKIKKDASEELK 298

Query 352 ILQKVNHGNIIVKLMGVSSDNDGNCFFVVEYAENGSLLEEWLFAKSCSETSNRSTSLTWCQR 411


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Sbjct	299	ILQKVNHGHNVLKLMGVSSDNDGNCFLVYVEYAENGSLLEEWLF++S S+TSNS SLTW QR	357
Query	412	ISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKID	471
Sbjct	358	ITIAMDVAIGLQYMHEHTYPRIIHRDITSSNILLGSNFKAKIANFGMARTSTNSMMPKID	417
Query	472	VFAFGVVLIELLTGKAMTTKENGGEVVMLWKDIWKIFDQENREERLRKWMDPKLDNYYP	531
Sbjct	418	VFAFGVVLIELLTG+KAMTTKENGGEVV+LWKD WKIFD E NREERLRKWMDPKL+++YP	477
Query	532	IDYALSLAS 540	
Sbjct	478	IDNALSAS 486	

>emb|CA002966.1| LysM-domain containing receptor-like kinase [Medicago tornata]
Length=487

Score = 718 bits (1853), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 349/489 (71%), Positives = 411/489 (84%), Gaps = 4/489 (0%)

Query	53	YISQSPNFLSLTSSVSNIFDTSPLSIARASNLOHEEDKLIPGQVLLIPVTCGCTGNRSFAN	112
Sbjct	1	Y+QSPNFLSL++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTGCT N SFAN	60
Query	113	ISYEINGQDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQL	172
Sbjct	61	I+Y I GD+P++ T YQNLTN+ + NP LS LP+ +V +PLFCKCPSKNQL	120
Query	173	DRGIKYLITTHVWQPNNDVSVSNKLGASPDILSENNYGQNF+TAASNLPVLIPVTLPLDL	232
Sbjct	121	++GIKYLIT+VWQ QNDNV+ VS+K GAS ++L+ENN+ NFTA+N VLIPVT LP L	178
Query	233	IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLVVCVCLMKMKSINRSASSAETADKL	291
Sbjct	179	Q S+GRK L +IIGISLG ++V + LV V CLKMK LNRS SS+ETADKL	238
Query	292	LSGVSGVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK	351
Sbjct	239	LSGVSGVSKPTMYE AI+E TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK	298
Query	352	ILQKVNHGHNVLKLMGVSSDNDGNCFLVYVEYAENGSLLEEWLFAKSCSETSNRSSTLTWCQR	411
Sbjct	299	ILQKVNHGHNVLKLMGVSSDNDGNCFLVYVEYAENGSLLEEWLF++S S+TSNS SL+W QR	357
Query	412	ISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKID	471
Sbjct	358	ITIAMDVAIGLQYMHEHTYPRIIHRDITSSNILLGSNFKAKIANFGMARTSTNSMMPKID	417
Query	472	VFAFGVVLIELLTGKAMTTKENGGEVVMLWKDIWKIFDQENREERLRKWMDPKLDNYYP	531
Sbjct	418	VFAFGVVLIELLTG+KAMTTKENGGEVV+LWKD WKIFD E NREERLRKWMDPKL+++YP	477
Query	532	IDYALSLAS 540	
Sbjct	478	IDNALSAS 486	

>dbj|BAI79275.1|  LysM type receptor kinase [Lotus japonicus]



dbj|BAI79285.1|  LysM type receptor kinase [Lotus japonicus]
Length=591

GENE ID: 100380877 LYS11 | LysM type receptor kinase [Lotus japonicus]
(10 or fewer PubMed links)

Score = 706 bits (1823), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 370/606 (61%), Positives = 462/606 (76%), Gaps = 24/606 (3%)

Query	1	MAVFFVSLTLGAQILYVVMFFTC---IEAQSQQTNGTNFSCPSNSPPSCETYVITYISQS	57
Sbjct	1	M SF+ + ++MFF+ I AQ TNGTNFSCP +SPPSC+TYVITY +QS	57
Query	58	PNFLSLTSSVSNIFDTSPLSIARASNLOHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEI	117
Sbjct	58	PNFL+LTS+S++FDTSPLSIARASN++ E L+PGQ+LL+PVTC C+G+ SF+NIS+ I	117
Query	118	NQGDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIK	177
Sbjct	118	+G+S+Y+++TT Y+NLTNW V D NP + + LP+GI+VVIPLFCKCPS L++GI+	177
Query	178	YLIT+VW QNDNVSV+K G S QDI+SENN+ QNF+TAA+N P+LIPVT LP L QS	236
Sbjct	178	YLITYVWHNNNDVSVLASKFGVSTQDI+SENNF+SHQNF+TAA+NFP+LIPVTQLP+LSQS	237
Query	237	SDGRKRIHGLPVIIGISLGCTLLVVVSAIL-LVCVCCCLKMK--SLNRSASSAETA-DKLL	292
Sbjct	238	S + R II ++ A+L LV V CL+ + S N+S S E A KL+	297
Query	293	SGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK	352
Sbjct	298	SGVS YSK +YE I+EAT+NL+EQCKIGESVYKA ++G+VLAVK+ KEDVTEE+ I	357
Query	353	LQKVNHGHNVLKLMGVSSDNDGNCFLVYVEYAENGSLLEEWLFAKSCSETSNRSSTLTWCQR	412
Sbjct	358	LQKVNHNHNLVKLGMVSSGHDGNHFLVYFAENGSLHNWLF+ S ++ SR LTW QRI	413
Query	413	SIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKID	472
Sbjct	414	SIAVDVAMGLQYMHEHTQPSIVHRDITSSNILLDSNFKAKIANFSVARTSINPMILKVDV	473
Query	473	FAGVVLIELLTGKAMTTKENGGEVVMLWKDIWKIFDQENREERLRKWMDPKLDNYYP	532
Sbjct	474	I+G+VVLIELLTG+KAMTTKENGGEVV+LWKD WKIFD E NREERLRKWMDPKL+++YP	526
Query	533	DYALSLASLAVNCTADKSLSRPTIAEIVLSLSLL-TQPSPATLERSLTSSGLDVEATQIV	591
		D ALSLA LA+NCT++K LSRPT+ E+VLSLSLL TQ SP TLERS T GLDV+ T++	


Sbjct 527 DDALSLAFLAMNCTSEKPLSRPTMGEVVLSSLMLTQHSPTTLERSWT-CGLDVDVTEMQ 585
Query 592 TSISAR 597
T I+AR
Sbjct 586 TLIAAR 591

>ref|XP_002269472.1|  PREDICTED: hypothetical protein [Vitis vinifera]
emb|CB117584.3|  unnamed protein product [Vitis vinifera]
Length=590

GENE ID: 100259809 LOC100259809 | hypothetical protein LOC100259809
[Vitis vinifera] (10 or fewer PubMed links)

Score = 643 bits (1659), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 329/575 (57%), Positives = 420/575 (73%), Gaps = 6/575 (1%)

Query 25 IEAQSQQTNGTNFSCPSNSPPSCETYVYIISQSPNFLSLTSVSNIFDTSPLSIARASNLIQ 84
I AQS T TNFSC ++SP SC+TYV Y +Q+P FL + ++S++F S LSIA ASNL
Sbjct 20 ITAQSPATPVTNFSCCTDSPASCQTYVIYRAQAPGFLDVGNISDLFGISRLSIAEASNLA 79
Query 85 HEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSFYFVATTLYQNLTNWHAVMDLN 144
EE +L P Q+LL+P+ C CTGN FANI+Y+I DSFYFV+ T++NLTN++AV LN
Sbjct 80 SEEARLSPDQLLLVPLILCCTGNHYFANITYKIKTDDSFYFVSVTFENLTNYNAVEALN 139
Query 145 PGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHVWQPNDNVSVSNKLGASPDQI 204
PGL TL +G++VV PLFCKCPSK+ D+GI YLIT+VWQP D+V V L ASP DI
Sbjct 140 PGLPTTLQVGEVVFPLFCKCPSKSHSDKGINYLITYVWQPGDDVLLVGTNLKASPVDI 199
Query 205 LSENNYQGNFTAASNLPVLIPVTLPLDQSPSDGRKHRIGLPVIGISLGCTLLVVVSA 264
ENN NF+A+ + PVLIPV+ P L Q K R L +++ S G L+ ++ +
Sbjct 200 RDENN-NLNFASASVDQPVLPVSPQPLLTQFERRASKGRWILALVL--STGALLIFLLVS 256
Query 265 ILLVCVCLKMKSLNRSASSAETAD--KLLSGVSGYVSKPTMYETGAILEATMNLSEQCK 322
+L+ K K+L+ S SS ET D KLL GVSGY+ KP MYET I+EATMNL+E +
Sbjct 257 LLVYTGLIRKKKTLDHSESSLETTDLIKLLPGVSGYLGKPIMYETKVIMEATMNLNEHYR 316
Query 323 IGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNNLVKLMGVSSDNDGNCFFVVEYA 382
IG SVY+A I G+V+AVK+ KED+TEEL+ILQKVNHGNNLVKLMGVSSD DGN F+VVE+A
Sbjct 317 IGGSVYRATINGQVVAVKTKEDITEELRLQKVNHGNNLVKLMGVSSDADGNRFLVYEFA 376
Query 383 ENGSLLEWLFKASCSETSNRSRTSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSN 442
ENGSL++WL K S +S+ LTW QRI +A+DV+ GLQYMHEH P +VHRDI ++N
Sbjct 377 ENGSLDKWLHFKPSSPSSSV-AFLTWSQRQVQVLDVANGLYQMEHTQPSVVHRDIRANN 435
Query 443 ILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGVVLIELLTGRKAMTTKENGEEVVMWLK 502
ILLDS FKAKIANFSMA N MM K+DVFAFGVVL+ELL+G+KAM + NGE+VVMWLK
Sbjct 436 ILLDSRFKAKIANFSMATPAMNSMMPKVDVFAFGVVLLELLSGKKAMQMRANGEIVMLWK 495
Query 503 DIWKIFDQENREERLRKWMDPKLDNYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLS 562
DI +I + E+ RE+R+R+WMDP L+N+YP D AL+LA LA +CT +KS +RP++AEI +
Sbjct 496 DIREILEVEDEKREDRIRRWMDPTLENFYPFDGALNLAGLARSCTQEKSSARPSMAEIAFN 555
Query 563 LSLLTQSPATLERSLTSSGLDVEATQIVTSISAR 597
LS+L+Q S TTERS T E QI+ + AR
Sbjct 556 LSVLSQTSSETLERSWTQGFEPETIQIINPVIAR 590

>ref|XP_002533280.1|  serine-threonine protein kinase, plant-type, putative [Ricinus communis]
gb|EEF29112.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]
Length=620

GENE ID: 8272992 RCOM_0411680 | serine-threonine protein kinase, plant-type,
putative [Ricinus communis]

Score = 618 bits (1594), Expect = 6e-175, Method: Compositional matrix adjust.
Identities = 330/602 (54%), Positives = 420/602 (69%), Gaps = 32/602 (5%)

Query 23 TCIEAQSQQTNGTNFSCPSNSPPSCETYVYIISQSPNFLSLTSVSNIFDTSPLSIARASN 82
I AQS Q GTNFSC + P C+TYV Y +Q PNFL+L ++S++F S LSIA ASN
Sbjct 24 TYVTAQSPQ--GTNFSCSVLDLSPCQTYVAYYAPQPNFLNLGNISDLFAVSRLSIASASN 81
Query 83 LQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSFYFVATTLYQNLTNWHAVMD 142
L E+ L+P Q+LL+P+TCGCTGN SFANI+Y+I GDSFYFV+TT ++NL W AV
Sbjct 82 LVSEDIPLMPNQLLLVPIITCGCTGNSSFANITYQIKPGDSFYFVSTTYFENLAKWQAVES 141
Query 143 LNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHVWQPNDNVSVSNKLGASPO 202
NP L L G +VV PLFCKCPSKNQ+ GI+YLIT+VWQP D++ V K ASP
Sbjct 142 FNPNDLPTLLHPGDKVVFPLFCKCPSKNQMKHGIQYLITYVWQPEDDIFKVGAKFNASPH 201
Query 203 DILSENNYQGNFTAASNLPVLIPVTLPLDQSPSDGRKHRIGLPVIGISLGCTLLVV 261
DI +NNY +F+ A + P+LIPVT +P L Q SPS ++ L +II S+ LL+
Sbjct 202 DIAIQNNYW-DFSTAVHHPLLPVTQMPILSQSPSPWQREHHLVIIIVTSVAGALLIF 260
Query 262 VSAILLV---CVCCCLKMK--SLNRSASSAETA-----DKLLSGVS 296
+ LV C C K K +L+R+ S ET DKLL GVS
Sbjct 261 LLVAFVLVHAHCCKKKKMTLHRNGSCLETTDLLQIKEQGKYRSFEPKIIQDKLLPGVS 320
Query 297 GYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKV 356
GY+ KP MY+ IL ATM+L E +IG SVY+ANI G+VLAVK+ K D+TEEL ILQKV
Sbjct 321 GYLKGPIMYDIKEILLATMDLHEHYRIGGSVYRANINGQVLAVKKTVDITEELNILQKV 380
Query 357 NHGNLVKLMGVSSDNDGNCFFVVEYAENGSLLEWLFKASCSETSNRSRTSLTWCQRISIAV 416
NH NLVKLMG+SS+ DG+CF+VVEYAENGSL++WL K + +S+S L+W QR+ IA+
Sbjct 381 NHANLVKLMGISSNADGDCFLVVEYAENGSLDKWLHPKP-ASSSSSVAFLSWSQRLQIAL 439
Query 417 DVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFG 476
DV+ GLQYMHEH P +VH DI +SNILLDS FKAKIANFS+A+ T+ M+ K+DVFAFG
Sbjct 440 DVASGLQYMHEHIQPTVHMDIRTSNILLDSRFKAKIANFSVAKLTDSMLQKVDVFAFG 499
Query 477 VVLIELLTGRKAMTTKENGEEVVMWLKDIWKIFDQENREERLRKWMDPKLDNYYPIDYAL 536
VVL+ELL G+KAM T ENGE+V+LWK++ + + E R ERL+K MDP L+N+YPID AL
Sbjct 500 VVLEELLCGKKAMVTNENGEIVLLWKEMKGMVEAEKRAERLRKMDPNLENFYPIDSAI 559


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Query 537 SLASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATLERSLTSSGLDVEA-TQIVTSIS 595
          SLA+LA CT +KS +RP++AEIV +L++LTQ T LERS T SGL+ E QI + +
Sbjct 560 SLANLARVCTLEKSSARPSMAEIVFNLTVLVTQSCSETLERSWT-SGLEAEEDIQITSPVI 618

Query 596 AR 597
          AR
Sbjct 619 AR 620

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>ref|XP_002310198.1|  predicted protein [Populus trichocarpa]

gb|EEE90648.1|  predicted protein [Populus trichocarpa]
Length=601

GENE ID: 7473142 POPTRDRAFT_870366 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score = 595 bits (1534), Expect = 7e-168, Method: Compositional matrix adjust.
Identities = 321/607 (52%), Positives = 425/607 (70%), Gaps = 16/607 (2%)

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Query 1 MAVFFVSLTLGAQILYVVLMEFTCIAEQSQQTNGTNFSCPSNSPPSCETYVTVYISQSPNF 60
          MA+ +S + ++VL+FF+ +Q GTNFSCP +SP SC TY++Y++Q P+P
Sbjct 1 MAISLLSFFFTQALFFVLVLFSTY-VTAQAPPCTNFSCPVDSTSCPTYISYLAQPPDF 59

Query 61 LSLTSSVSNIFDTSPLSIARASNLOHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQG 120
          L L +S++F S IA ASNL E+ L P Q+LL+P+ CGCTG++SF NI+Y+I QG
Sbjct 60 LDLGKISHLFGISRTLIASASNLVSEDTPLFPNQLLLVPIRCGCTGSQSFVNITYQIQQG 119

Query 121 DSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYL 180
          DS Y V+T ++NLT W V LN L+ L G +V+ PLFCKCPS+ L+ GI++LI
Sbjct 120 DSYSVSTISFENLTRWQVEALNRS LPTLLHAGDEVIFPLFCKCPSRTHLENGIEHLI 179

Query 181 THVWQPNNDNVSFVSNKLGASPDILSENNGQNFTAASNLFVLIPTVLLPDLIQ---SPS 237
          T+VWQP D++ V+ L AS ++I+ ENNY NF AA P++IPV+ LP L Q +P
Sbjct 180 TYVWQPGDDLKKVAAMLNASERNIVNIENNY-DNFNAAVYNPIVIPVSKLPVLSQPYLTPE 238

Query 238 D-GRKHRIGLFPVIIGISLGLCTLLVV-VSAILLVCCCLK-MKSLNRSASSAETAD--KLL 292
          G KH --VI+ S+ T + A L+ C K K+L+R+ S ET+D KLL
Sbjct 239 RRGSKHL--WIVIVAASIASTFFTCPLVAFLIHKRCSYKATKALDRTGSCLETSDDPKLL 296

Query 293 SGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKI 352
          GV G + K +YE AI+E TM+L E KIG SVY+ANI G VLAVK+ K+DVTEELKI
Sbjct 297 PGVLGCLDKSIIIEVKAIMEGTMDLHEHYKIGGSVYRANINGCVLAVKTKDDVTEELKI 356

Query 353 LQKVNHNGLVKLMGVSSDND--GNCFVVEYAENGSLLEEWLFAKSCSETSNRSTSLTWCQ 410
          LQKV+H NLVKLMG+SS++D GN F+VVEYAENGSL++WL KS +S+S LTW Q
Sbjct 357 LQKVSHANLVKLMGMSSESDREGNRFVVEYAENGSLDKWLHPKS-ESSSSSVGFLTWKQ 415


Query 411 RISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKI 470
          R+ +A+DV+ GLQY+HEH PR VH+DI +SNILLDS F+AKIANFSMAR T+ MM K
Sbjct 416 RMQVALDVANGLQYLHEHTQPRTVHKDIRTSNILLDSTFRAKIANFSMARAATDSMMPKD 475

Query 471 DVFAFGVVLIELLTGRKAMTKENGVEVVMWLKDIWKIFDQEEENREERLRKWMDFKLDNYY 530
          DVFFGVVL+ELL+G+KAM TKE GE+V+L ++I + + EE REERLRKWMDF L+ +Y
Sbjct 476 DVFDGFGVVLLELLSGKKAMVTKEKGEIVLLCREIKDVLEMEEKREERLRKWMDFNLERFY 535

Query 531 PIDYALSASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATLERSLTSSGLDVEATQI 590
          PID A+SLA+LA CT +KS RP++AEIV +L++LTQ SP TLER TS + T++
Sbjct 536 PIDSAMS LATLARLCTLEKSSERPSMAEIVFNLTVLVTQSSPETLER-WTSEVETEDFTRL 594

Query 591 VTSISAR 597
          V+ ++AR
Sbjct 595 VSPVTAR 601

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>gb|ADJ19109.1|  truncated Nod-factor receptor 5A [Glycine max]
Length=337

GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
(10 or fewer PubMed links)

Score = 536 bits (1381), Expect = 4e-150, Method: Compositional matrix adjust.
Identities = 277/337 (82%), Positives = 301/337 (89%), Gaps = 1/337 (0%)

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Query 1 MAVFFVSLTLGAQILYVVLMEFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTVYISQSPN 59
          MAVFF L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTVYI+QSPN
Sbjct 1 MAVFFPPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDPPSCETYVTVYIAQSPN 60

Query 60 FLSLTSSVSNIFDTSPLSIARASNLOHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQ 119
          FLSLT++SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQ
Sbjct 61 FLSLTNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQ 120

Query 120 GDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYL 179
          GDSFYFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYL
Sbjct 121 GDSFYFVATTSYENLTNWRVMDLNPVLSPNKLPPIGIQVVFPLFCKCPSKNQLDKKIKYL 180

Query 180 ITHVWQPNNDNVSFVSNKLGASPDILSENNGQNFTAASNLFVLIPTVLLPDLIQSPSDG 239
          IT+VW+P DNVS VS+K GASP+DI+SENNGQNFTAASNLFVLIPTV L P L +SPSDG
Sbjct 181 ITYVWKPGDNVSLVSDKFGASPEDIMSENNGQNFTAANNLPVLIPTVTRLPVLARSPSDG 240

Query 240 RKHRIGLFPVIIGISLGLCTLLVVVSAILLVCCCLKMKSLNRSASSAETADKLLSGVSGYV 299
          RK I LPVIIGISLGLCTLLV+V A+LLV V CLKMK+LNRSSASSAETADKLLSGVSGYV
Sbjct 241 RKGGRILFPVIIGISLGLCTLLVLAVLLVYVYCLKMKT LNRSSASSAETADKLLSGVSGYV 300

Query 300 SKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKV 336
          SKPTMYET AI+EATMNLSEQCKIGESVYKANIEGKV
Sbjct 301 SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKV 337

```

>dbj|BAG85147.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 519 bits (1337), Expect = 4e-145, Method: Compositional matrix adjust.
Identities = 261/327 (79%), Positives = 285/327 (87%), Gaps = 1/327 (0%)

```

Query 5 FVSLTLGAQILYVVLMEFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTVYISQSPNFLSL 63
          F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTVYI+QSPNFLSL

```



```

Sbjct 1 FPFLLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPSCETYVVTYIAQSPNFLSL 60
Query 64 TSVSNI FDTSPLSIARASN LQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGD SF 123
T++SNI FDTSPLSIARASN L+ +DKL+ QVLL+PVT CGCTGNRSFAN SYEINQGD SF
Sbjct 61 TNISNI FDTSPLSIARASNLEPMD DKL VKDQVLLVPVTCGCTGNRSFANTSYEINQGD SF 120
Query 124 YFVATTLYQNLTNWHAVMDLNPGLSQFTLP IGIQVVIPLFCKCPSKNQLDRGIKYLITHV 183
YFVATT Y+NL TNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V
Sbjct 121 YFVATT SYENLTNWRVMDLNPVLS PNKLP IGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180
Query 184 WQPN DNVSVFSNKL GASPQDIL SENNYGQNFTAASNLPVLIPVTL LPDIQSPSDGRKHR 243
W+P DNVS VS+K GASP+DI+SEN NYGQNFTA A+NL PVLIPVT LP L +SPSDGRK
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNY GQNFTAANNLPVLIPVTRL PVLARSPSDGRKGG 240
Query 244 IGLPVIIGISLGCTLLVVVSAILLVCC LKMKSLNRSASSAETADKLLSGVSGYVSKPT 303
I LPVIIGI+LGCTLLV+V A CLKMK+LNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPVIIGITLGCTLLVLV LASYWAYGYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 300
Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
MYET AI+EATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

```

```

>dbj|BAG85143.1| Nod factor receptor protein [Glycine soja]
dbj|BAG85149.1| Nod factor receptor protein [Glycine soja]
dbj|BAG85156.1| Nod factor receptor protein [Glycine soja]
11 more sequence titles

```

```

dbj|BAG85159.1| Nod factor receptor protein [Glycine max]
dbj|BAG85160.1| Nod factor receptor protein [Glycine max]
dbj|BAG85161.1| Nod factor receptor protein [Glycine max]
dbj|BAG85162.1| Nod factor receptor protein [Glycine max]
dbj|BAG85165.1| Nod factor receptor protein [Glycine max]
dbj|BAG85168.1| Nod factor receptor protein [Glycine max]
dbj|BAG85171.1| Nod factor receptor protein [Glycine max]
dbj|BAG85174.1| Nod factor receptor protein [Glycine max]
dbj|BAG85177.1| Nod factor receptor protein [Glycine max]
dbj|BAG85179.1| Nod factor receptor protein [Glycine max]
dbj|BAG85180.1| Nod factor receptor protein [Glycine max]
Length=327

```

Score = 516 bits (1329), Expect = 3e-144, Method: Compositional matrix adjust.
Identities = 267/327 (81%), Positives = 291/327 (88%), Gaps = 1/327 (0%)

```

Query 5 FVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVVTYISQSPNFLSL 63
F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVVTYI+QSPNFLSL
Sbjct 1 FPFLLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPSCETYVVTYIAQSPNFLSL 60
Query 64 TSVSNI FDTSPLSIARASN LQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGD SF 123
T++SNI FDTSPLSIARASN L+ +DKL+ QVLL+PVT CGCTGNRSFANISYEINQGD SF
Sbjct 61 TNISNI FDTSPLSIARASNLEPMD DKL VKDQVLLVPVTCGCTGNRSFANISYEINQGD SF 120
Query 124 YFVATTLYQNLTNWHAVMDLNPGLSQFTLP IGIQVVIPLFCKCPSKNQLDRGIKYLITHV 183
YFVATT Y+NL TNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V
Sbjct 121 YFVATT SYENLTNWRVMDLNPVLS PNKLP IGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180
Query 184 WQPN DNVSVFSNKL GASPQDIL SENNYGQNFTAASNLPVLIPVTL LPDIQSPSDGRKHR 243
W+P DNVS VS+K GASP+DI+SEN NYGQNFTA A+NL PVLIPVT LP L +SPSDGRK
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNY GQNFTAANNLPVLIPVTRL PVLARSPSDGRKGG 240
Query 244 IGLPVIIGISLGCTLLVVVSAILLVCC LKMKSLNRSASSAETADKLLSGVSGYVSKPT 303
I LPVIIGISLGCTLLV+V A+LLV V CLKMK+LNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPVIIGISLGCTLLVLV LAVLLVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 300
Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
MYET AI+EATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

```

```

>dbj|BAG85152.1| Nod factor receptor protein [Glycine soja]
Length=327

```

Score = 516 bits (1328), Expect = 5e-144, Method: Compositional matrix adjust.
Identities = 267/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

```

Query 5 FVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVVTYISQSPNFLSL 63
F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVVTYI+QSPNFLSL
Sbjct 1 FPFLLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPSCETYVVTYIAQSPNFLSL 60
Query 64 TSVSNI FDTSPLSIARASN LQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGD SF 123
T++SNI FDTSPLSIARASN L+ +DKL+ QVLL+PVT CGCTGNRSFANISYEINQGD SF
Sbjct 61 TNISNI FDTSPLSIARASNLEPMD DKL VKDQVLLVPVTCGCTGNRSFANISYEINQGD SF 120
Query 124 YFVATTLYQNLTNWHAVMDLNPGLSQFTLP IGIQVVIPLFCKCPSKNQLDRGIKYLITHV 183
YFVATT Y+NL TNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V
Sbjct 121 YFVATT SYENLTNWRVMDLNPVLS PNKLP IGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180
Query 184 WQPN DNVSVFSNKL GASPQDIL SENNYGQNFTAASNLPVLIPVTL LPDIQSPSDGRKHR 243
W+P DNVS VS+K GASP+DI+SEN NYGQNFTA A+NL PVLIPVT LP L +SPSDGRK
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNY GQNFTAANNLPVLIPVTRL PVLARSPSDGRKGG 240
Query 244 IGLPVIIGISLGCTLLVVVSAILLVCC LKMKSLNRSASSAETADKLLSGVSGYVSKPT 303
I LPVIIGISLGCTLLV V A+LLV V CLKMK+LNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPVIIGISLGCTLLVQVLAVLLVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 300
Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
MYET AI+EATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

```

```

>dbj|BAG85148.1| Nod factor receptor protein [Glycine soja]
Length=327

```


Score = 515 bits (1327), Expect = 5e-144, Method: Compositional matrix adjust.
Identities = 266/327 (81%), Positives = 291/327 (88%), Gaps = 1/327 (0%)

```

Query 5 FVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVVTYISQSPNFLSL 63

```

```
Sbjct 1 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL 60
        FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPPSCETYVTYIAQSPNFLSL
Query 64 TSVSNI FDTSPLSIARASN LQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSE 123
        T++SNIFDTSPLS+ARASN L+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDSE
Sbjct 61 TNISNIFDTSPLSVARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE 120
        TNISNIFDTSPLSVARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE
Query 124 YFVATTLYQNLTNWHAVMDLNPGLSQFTLP IGIQVVIPLFCKCPSKNQLDRGIKYLITHV 183
        YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V
Sbjct 121 YFVATTSYENLTNWRVMDLNPVLSPNKLP IGIQVVPFPLFCKCPSKNQLDKEIKYLITYV 180
        YFVATTSYENLTNWRVMDLNPVLSPNKLP IGIQVVPFPLFCKCPSKNQLDKEIKYLITYV
Query 184 WQPNDNVSFVS NKL GASPQDILSEN NYGNFTAA SNLPVLIPVTL LLDLIQSPSDGRKHR 243
        W+P DNVS VS+K GASP+DI+SEN NYGNFTAA+NL PVLIPVT LP L +SPSDGRK
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSEN NYGNFTAA NNLPVLIPVTRLPVLARS PSDGRKGG 240
        WKPGDNVSLVSDKFGASPEDIMSEN NYGNFTAA NNLPVLIPVTRLPVLARS PSDGRKGG
Query 244 IGLPVIIGISLGCTLLVVVSAILLVCCCLMKKSLNRSASSAETADKLLSGVSGYVSKPT 303
        I LPVIIGISLGCTLLV+V A+LLV V CLKMK+LNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKT LNRSASSAETADKLLSGVSGYVSKPT 300
        IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKT LNRSASSAETADKLLSGVSGYVSKPT
Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
        MYET AI+EATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
        MYETDAIMEATMNLSEQCKIGESVYKA
```

>dbj|BAG85178.1|  Nod factor receptor protein [Glycine max]
Length=327

GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
(10 or fewer PubMed links)

Score = 514 bits (1325), Expect = 9e-144, Method: Compositional matrix adjust.
Identities = 266/327 (81%), Positives = 291/327 (88%), Gaps = 1/327 (0%)

```
Query 5 FVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL 63
        F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL
Sbjct 1 FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPPSCETYVTYIAQSPNFLSL 60
        FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPPSCETYVTYIAQSPNFLSL
Query 64 TSVSNI FDTSPLSIARASN LQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSE 123
        T++SNIFDT+PLSIARASN L+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDSE
Sbjct 61 TNISNIFDTNPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE 120
        TNISNIFDTNPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE
Query 124 YFVATTLYQNLTNWHAVMDLNPGLSQFTLP IGIQVVIPLFCKCPSKNQLDRGIKYLITHV 183
        YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V
Sbjct 121 YFVATTSYENLTNWRVMDLNPVLSPNKLP IGIQVVPFPLFCKCPSKNQLDKEIKYLITYV 180
        YFVATTSYENLTNWRVMDLNPVLSPNKLP IGIQVVPFPLFCKCPSKNQLDKEIKYLITYV
Query 184 WQPNDNVSFVS NKL GASPQDILSEN NYGNFTAA SNLPVLIPVTL LLDLIQSPSDGRKHR 243
        W+P DNVS VS+K GASP+DI+SEN NYGNFTAA+NL PVLIPVT LP L +SPSDGRK
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSEN NYGNFTAA NNLPVLIPVTRLPVLARS PSDGRKGG 240
        WKPGDNVSLVSDKFGASPEDIMSEN NYGNFTAA NNLPVLIPVTRLPVLARS PSDGRKGG
Query 244 IGLPVIIGISLGCTLLVVVSAILLVCCCLMKKSLNRSASSAETADKLLSGVSGYVSKPT 303
        I LPVIIGISLGCTLLV+V A+LLV V CLKMK+LNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKT LNRSASSAETADKLLSGVSGYVSKPT 300
        IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKT LNRSASSAETADKLLSGVSGYVSKPT
Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
        MYET AI+EATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
        MYETDAIMEATMNLSEQCKIGESVYKA
```

>dbj|BAG85144.1| Nod factor receptor protein [Glycine soja]
>dbj|BAG85145.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 514 bits (1325), Expect = 1e-143, Method: Compositional matrix adjust.
Identities = 267/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

```
Query 5 FVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL 63
        F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL
Sbjct 1 FPFPLPLHFQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPPSCETYVTYIAQSPNFLSL 60
        FPFPLPLHFQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPPSCETYVTYIAQSPNFLSL
Query 64 TSVSNI FDTSPLSIARASN LQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSE 123
        T++SNIFDTSPLSIARASN L+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDSE
Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE 120
        TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE
Query 124 YFVATTLYQNLTNWHAVMDLNPGLSQFTLP IGIQVVIPLFCKCPSKNQLDRGIKYLITHV 183
        YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V
Sbjct 121 YFVATTSYENLTNWRVMDLNPVLSPNKLP IGIQVVPFPLFCKCPSKNQLDKEIKYLITYV 180
        YFVATTSYENLTNWRVMDLNPVLSPNKLP IGIQVVPFPLFCKCPSKNQLDKEIKYLITYV
Query 184 WQPNDNVSFVS NKL GASPQDILSEN NYGNFTAA SNLPVLIPVTL LLDLIQSPSDGRKHR 243
        W+P DNVS VS+K GASP+DI+SEN NYGNFTAA+NL PVLIPVT LP L +SPSDGRK
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSEN NYGNFTAA NNLPVLIPVTRLPVLARS PSDGRKGG 240
        WKPGDNVSLVSDKFGASPEDIMSEN NYGNFTAA NNLPVLIPVTRLPVLARS PSDGRKGG
Query 244 IGLPVIIGISLGCTLLVVVSAILLVCCCLMKKSLNRSASSAETADKLLSGVSGYVSKPT 303
        I LPVIIGISLGCTLLV+V A+LLV V CLKMK+LNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKT LNRSASSAETADKLLSGVSGYVSKPT 300
        IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKT LNRSASSAETADKLLSGVSGYVSKPT
Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
        MYET AI+EATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
        MYETDAIMEATMNLSEQCKIGESVYKA
```

>dbj|BAG85170.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 514 bits (1325), Expect = 1e-143, Method: Compositional matrix adjust.
Identities = 266/327 (81%), Positives = 291/327 (88%), Gaps = 1/327 (0%)

```
Query 5 FVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL 63
        F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL
Sbjct 1 FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPPSCETYVTYIAQSPNFLSL 60
        FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPPSCETYVTYIAQSPNFLSL
Query 64 TSVSNI FDTSPLSIARASN LQHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSE 123
        T++SNIFDTSPLSIARASN L+ +DKL+ QVLL+PVTGCTGNRSFA+ISYEINQGDSE
Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFADISYEINQGDSE 120
        TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFADISYEINQGDSE
Query 124 YFVATTLYQNLTNWHAVMDLNPGLSQFTLP IGIQVVIPLFCKCPSKNQLDRGIKYLITHV 183
        YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V
Sbjct 121 YFVATTSYENLTNWRVMDLNPVLSPNKLP IGIQVVPFPLFCKCPSKNQLDKEIKYLITYV 180
        YFVATTSYENLTNWRVMDLNPVLSPNKLP IGIQVVPFPLFCKCPSKNQLDKEIKYLITYV
```

```
Query 184 WQPNNDVSVFVSNKLGASPDILSENNYQNFNTAASNLPVLIPVTLTLLPDLIQSPSDGRKHR 243
Sbjct 181 WKPGDNVSVLSVDKFGASPDIMSENNYQNFNTAANNLPVLIPVTRLVPLARSPSDGRKGG 240

Query 244 IGLPVIIGISLGCCTLLVVVSAILLVCVCCCLKMKSLNRSASSAETADKLLSGVSGYVSKPT 303
Sbjct 241 IRLPVIIGISLGCCTLLVVLAVLLVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
```

>dbj|BAG85167.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 514 bits (1325), Expect = 1e-143, Method: Compositional matrix adjust.
Identities = 266/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

```
Query 5 FVSLTLGAQILYVVMFF-TCIEAQSQQTNFTNFSCPSNSPPSCETYVTYISQSPNFLSL 63
Sbjct 1 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL 60
FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL

Query 64 TSVSNIFFDTSPLSIARASNLOHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSE 123
Sbjct 61 ++SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTCGCTGNRSFANISYEINQGDSE 120
ANISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE

Query 124 YFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHV 183
Sbjct 121 YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V 180
YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQLDKEIKYLITYV

Query 184 WQPNNDVSVFVSNKLGASPDILSENNYQNFNTAASNLPVLIPVTLTLLPDLIQSPSDGRKHR 243
Sbjct 181 WKPGDNVSVLSVDKFGASPDIMSENNYQNFNTAANNLPVLIPVTRLVPLARSPSDGRKGG 240

Query 244 IGLPVIIGISLGCCTLLVVVSAILLVCVCCCLKMKSLNRSASSAETADKLLSGVSGYVSKPT 303
Sbjct 241 IRLPVIIGISLGCCTLLVVLAVLLVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
```

>dbj|BAG85164.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 514 bits (1325), Expect = 1e-143, Method: Compositional matrix adjust.
Identities = 266/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

```
Query 5 FVSLTLGAQILYVVMFF-TCIEAQSQQTNFTNFSCPSNSPPSCETYVTYISQSPNFLSL 63
Sbjct 1 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL 60
FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL

Query 64 TSVSNIFFDTSPLSIARASNLOHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSE 123
Sbjct 61 T++SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTCGCTGNRSFANISYEINQGDSE 120
TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE

Query 124 YFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHV 183
Sbjct 121 YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V 180
YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQLDKEIKYLITYV

Query 184 WQPNNDVSVFVSNKLGASPDILSENNYQNFNTAASNLPVLIPVTLTLLPDLIQSPSDGRKHR 243
Sbjct 181 WKPGDNVSVLSVDKFGASPDIMSENNYQNFNTAANNLPVLIPVTRLVPLARSPSDGRKGG 240

Query 244 IGLPVIIGISLGCCTLLVVVSAILLVCVCCCLKMKSLNRSASSAETADKLLSGVSGYVSKPT 303
Sbjct 241 IRLPVIIGISLGCCTLLVVLAVLLVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
Sbjct 301 MYEADIMEATMNLSEQCKIGESVYKA 327
```

>dbj|BAG85151.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 514 bits (1324), Expect = 1e-143, Method: Compositional matrix adjust.
Identities = 266/327 (81%), Positives = 291/327 (88%), Gaps = 1/327 (0%)

```
Query 5 FVSLTLGAQILYVVMFF-TCIEAQSQQTNFTNFSCPSNSPPSCETYVTYISQSPNFLSL 63
Sbjct 1 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL 60
FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL

Query 64 TSVSNIFFDTSPLSIARASNLOHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSE 123
Sbjct 61 T++SNIF+TSPLSIARASNL+ +DKL+ QVLL+PVTCGCTGNRSFANISYEINQGDSE 120
TNISNIFETSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE

Query 124 YFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHV 183
Sbjct 121 YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V 180
YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQLDKEIKYLITYV

Query 184 WQPNNDVSVFVSNKLGASPDILSENNYQNFNTAASNLPVLIPVTLTLLPDLIQSPSDGRKHR 243
Sbjct 181 WKPGDNVSVLSVDKFGASPDIMSENNYQNFNTAANNLPVLIPVTRLVPLARSPSDGRKGG 240

Query 244 IGLPVIIGISLGCCTLLVVVSAILLVCVCCCLKMKSLNRSASSAETADKLLSGVSGYVSKPT 303
Sbjct 241 IRLPVIIGISLGCCTLLVVLAVLLVYVYCLKMKTLNRSASSAETADKLLSGVSGYVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
```

>dbj|BAG85146.1| Nod factor receptor protein [Glycine soja]

Length=327

Score = 514 bits (1324), Expect = 1e-143, Method: Compositional matrix adjust.
Identities = 266/327 (81%), Positives = 291/327 (88%), Gaps = 1/327 (0%)


Query	5	FVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL	63
		F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL	
Sbjct	1	FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL	60
Query	64	TSVSNIFDTSPLSIARASNLCHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSE	123
		T++SNIFDTSPLSIARASNLC +DKL+ QVLL+PVTCGCTGNRSFANISYEINQGDSE	
Sbjct	61	TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE	120
Query	124	YFVATTLYQNLTNWHAVMMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHV	183
		YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V	
Sbjct	121	YFVATTSYENLTNWRVMDLNPVLSNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	180
Query	184	WQPDNDVSFVSNKLGASPDILSENNGQNFATAASNLPVLIPVTLPLDQSPSDGRKRR	243
		W+P DNVS VS+K GASP+DI+SENNGQNFATA+NLFPVLIPVT LP L +SPSDGRK	
Sbjct	181	WKPGDNVSLVSDKFGASPDIMSENNGQNFATAANNLPVLIPVTRLPLVLARSPSDGRKGG	240
Query	244	IGLPVIGISLGTLLVVSAILLVCCCLMKKSLNRSASSAETADKLLSGVSGYVSKPT	303
		I LPVIGISLGTLLV+V A+LLV V CLKMK+LNRSASSAETADKLLSGVSGYVSKPT	
Sbjct	241	IRLPVIGISLGTLLVLVLAVLLVYVYCLKMKT LNRSASSAETADKLLSGVSGYVSKPT	300
Query	304	MYETGAILEATMNLSEQCKIGESVYKA 330	
		+YET AI+EATMNLSEQCKIGESVYKA	
Sbjct	301	VYETDAIMEATMNLSEQCKIGESVYKA 327	

>dbj|BAG85153.1| Nod factor receptor protein [Glycine soja]

Length=327

Score = 514 bits (1323), Expect = 2e-143, Method: Compositional matrix adjust.
Identities = 266/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query	5	FVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL	63
		F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL	
Sbjct	1	FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL	60
Query	64	TSVSNIFDTSPLSIARASNLCHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSE	123
		T++SNIFDTSPLSIARASNLC +DKL+ QVLL+PVTCGCTGNRSFANISYEINQGDSE	
Sbjct	61	TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE	120
Query	124	YFVATTLYQNLTNWHAVMMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHV	183
		YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V	
Sbjct	121	YFVATTSYENLTNWRVMDLNPVLSNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	180
Query	184	WQPDNDVSFVSNKLGASPDILSENNGQNFATAASNLPVLIPVTLPLDQSPSDGRKRR	243
		W+P DNVS VS+K GASP+DI+SENNGQNFATA+NLFPVLIPVT LP L +SPSDGRK	
Sbjct	181	WKPGDNVSLVSDKFGASPDIMSENNGQNFATAANNLPVLIPVTRLPLVLARSPSDGRKGG	240
Query	244	IGLPVIGISLGTLLVVSAILLVCCCLMKKSLNRSASSAETADKLLSGVSGYVSKPT	303
		I LPVIGISLGTLLV+V A+LLV V CLKMK+LNRSASSAETADKLLSGVSGYVSKPT	
Sbjct	241	IRLPVIGISLGTLLVLVLAVLLVYVYCLKMKT LNRSASSAETADKLLSGVSGYVSKPT	300
Query	304	MYETGAILEATMNLSEQCKIGESVYKA 330	
		MYET AI+EAT NLSEQCKIGESVYKA	
Sbjct	301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>dbj|BAG85158.1|  Nod factor receptor protein [Glycine max]

Length=327

GENE ID: 100301877 *nfr5a* | Nod factor receptor protein [Glycine max]
(10 or fewer PubMed links)

Score = 514 bits (1323), Expect = 2e-143, Method: Compositional matrix adjust.
Identities = 266/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query	5	FVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL	63
		F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL	
Sbjct	1	FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL	60
Query	64	TSVSNIFDTSPLSIARASNLCHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSE	123
		T++SNIFDTSPLSIARASNLC +DKL+ QVLL+PVTCGCTGNRSFANISYEINQGDSE	
Sbjct	61	TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE	120
Query	124	YFVATTLYQNLTNWHAVMMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHV	183
		YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V	
Sbjct	121	YFVATTSYENLTNWRVMDLNPVLSNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	180
Query	184	WQPDNDVSFVSNKLGASPDILSENNGQNFATAASNLPVLIPVTLPLDQSPSDGRKRR	243
		W+P DNVS VS+K GASP+DI+SENNGQNF AA+NLFPVLIPVT LP L +SPSDGRK	
Sbjct	181	WKPGDNVSLVSDKFGASPDIMSENNGQNFATAANNLPVLIPVTRLPLVLARSPSDGRKGG	240
Query	244	IGLPVIGISLGTLLVVSAILLVCCCLMKKSLNRSASSAETADKLLSGVSGYVSKPT	303
		I LPVIGISLGTLLV+V A+LLV V CLKMK+LNRSASSAETADKLLSGVSGYVSKPT	
Sbjct	241	IRLPVIGISLGTLLVLVLAVLLVYVYCLKMKT LNRSASSAETADKLLSGVSGYVSKPT	300
Query	304	MYETGAILEATMNLSEQCKIGESVYKA 330	
		MYET AI+EATMNLSEQCKIGESVYKA	
Sbjct	301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>dbj|BAG85172.1| Nod factor receptor protein [Glycine max]

Length=327

Score = 514 bits (1323), Expect = 2e-143, Method: Compositional matrix adjust.
Identities = 266/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query	5	FVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL	63
		F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL	
Sbjct	1	FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL	60
Query	64	TSVSNIFDTSPLSIARASNLCHEEDKLI PGQVLLIPVTCGCTGNRSFANISYEINQGDSE	123
		T++SNIFDTSPLSIARASNLC +DKL+ QVLL+PVTCGCTGNRSFANISYEINQGDSE	

```
Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120
Query 124 YFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVPLFCKCPSKNQLDRGIKYLITHV 183
YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V
Sbjct 121 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVPLFCKCPSKNQLDKEIKYLITYV 180
Query 184 WQPNNDVSVFSNKLGAQSPQDILSENNYGQNFATAASNLPVLIPVTLPLDQSPSDGRKHR 243
W+P DNVS VS+K GASP+DI+SENNYGQNFATA+N PVLIPVT LP L +SPSDGRK
Sbjct 181 WKPGDNVSVLSVDKFGASPEDIMSENNYGQNFATAANNPVLIPVTRLPLVLARSPSDGRKGG 240
Query 244 IGLPVIIGISLGCTLLVVVSAILLVCCCLMKMSLNRSASSAETADKLLSGVSGYVSKPT 303
I LPVIIGISLGCTLLV+V A+LLV V CLKMK+LNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKT LNRSASSAETADKLLSGVSGYVSKPT 300
Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
MYET AI+EATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
```

>dbj|BAG85142.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 513 bits (1322), Expect = 2e-143, Method: Compositional matrix adjust.
Identities = 266/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

```
Query 5 FVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVVTYISQSPNFLSL 63
F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVVTYI+QSPNFLSL
Sbjct 1 FPFPLPHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVVTYIAQSPNFLSL 60
Query 64 TSVSNIIDFTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 123
T++SNIFDTSPLSIARASN+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDSF
Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120
Query 124 YFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVPLFCKCPSKNQLDRGIKYLITHV 183
YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V
Sbjct 121 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVPLFCKCPSKNQLDKEIKYLITYV 180
Query 184 WQPNNDVSVFSNKLGAQSPQDILSENNYGQNFATAASNLPVLIPVTLPLDQSPSDGRKHR 243
W+P DNVS VS+K GASP+DI+SENNYGQNFATA+NLPVLIPVT LP L +SPSDGRK
Sbjct 181 WKPGDNVSVLSVDKFGASPEDIMSENNYGQNFATAANNPVLIPVTRLPLVLARSPSDGRKGG 240
Query 244 IGLPVIIGISLGCTLLVVVSAILLVCCCLMKMSLNRSASSAETADKLLSGVSGYVSKPT 303
I LPVIIGISLGCTLLV+V A+LLV V CLKMK+LNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKT LNRSASSAETADKLLSGVSGYVSKPT 300
Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
MYET AI+EATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
```

>dbj|BAG85175.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 513 bits (1321), Expect = 3e-143, Method: Compositional matrix adjust.
Identities = 265/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

```
Query 5 FVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVVTYISQSPNFLSL 63
F L L +QIL +V+M F T I AQSQQ N T F+CPS+SPPSCETYVVTYI+QSPNFLSL
Sbjct 1 FPFPLPHSQILCLVIMLFSTNIVAQSQQDNRTKFTCPDSPPSCETYVVTYIAQSPNFLSL 60
Query 64 TSVSNIIDFTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 123
T++SNIFDTSPLSIARASN+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDSF
Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120
Query 124 YFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVPLFCKCPSKNQLDRGIKYLITHV 183
YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V
Sbjct 121 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVPLFCKCPSKNQLDKEIKYLITYV 180
Query 184 WQPNNDVSVFSNKLGAQSPQDILSENNYGQNFATAASNLPVLIPVTLPLDQSPSDGRKHR 243
W+P DNVS VS+K GASP+DI+SENNYGQNFATA+NLPVLIPVT LP L +SPSDGRK
Sbjct 181 WKPGDNVSVLSVDKFGASPEDIMSENNYGQNFATAANNPVLIPVTRLPLVLARSPSDGRKGG 240
Query 244 IGLPVIIGISLGCTLLVVVSAILLVCCCLMKMSLNRSASSAETADKLLSGVSGYVSKPT 303
I LPVIIGISLGCTLLV+V A+LLV V CLKMK+LNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKT LNRSASSAETADKLLSGVSGYVSKPT 300
Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
MYET AI+EATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
```

>dbj|BAG85150.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 513 bits (1321), Expect = 3e-143, Method: Compositional matrix adjust.
Identities = 265/327 (81%), Positives = 289/327 (88%), Gaps = 1/327 (0%)

```
Query 5 FVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVVTYISQSPNFLSL 63
F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL
Sbjct 1 FPFPLPHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVVTYFAQSPNFLSL 60
Query 64 TSVSNIIDFTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 123
T++SNIFDTSPLSIARASN+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDSF
Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120
Query 124 YFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVPLFCKCPSKNQLDRGIKYLITHV 183
YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V
Sbjct 121 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVPLFCKCPSKNQLDKEIKYLITYV 180
Query 184 WQPNNDVSVFSNKLGAQSPQDILSENNYGQNFATAASNLPVLIPVTLPLDQSPSDGRKHR 243
W+P DNVS VS+K GASP+DI+SENNYGQNFATA+NLPVLIPVT LP L +SPSDGRK
Sbjct 181 WKPGDNVSVLSVDKFGASPEDIMSENNYGQNFATAANNPVLIPVTRLPLVLARSPSDGRKGG 240
Query 244 IGLPVIIGISLGCTLLVVVSAILLVCCCLMKMSLNRSASSAETADKLLSGVSGYVSKPT 303
I LP IIGISLGCTLLV+V A+LLV V CLKMK+LNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPAIIGISLGCTLLVLVLAVLLVYVYCLKMKT LNRSASSAETADKLLSGVSGYVSKPT 300
Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
```

Sbjct 301 MYET AI+EATMNLSEQCKIGESVYKA
MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BAG85173.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 513 bits (1320), Expect = 3e-143, Method: Compositional matrix adjust.
Identities = 265/327 (81%), Positives = 289/327 (88%), Gaps = 1/327 (0%)

Query 5	FVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL	63
	F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL	
Sbjct 1	FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL	60
Query 64	TSVSNIFDTSPLSIARASNLOHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSE	123
	T++SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDSE	
Sbjct 61	TNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQGDSE	120
Query 124	YFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHV	183
	YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V	
Sbjct 121	YFVATTSYENLTNWRVMDLNPVLSPNKLPPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	180
Query 184	WQPNDNVSFVSNKLGASPDILSENNGQNFATAASNLPVLIPVTLPLDQSPSDGRKHR	243
	W+P DNVS VS+K GASP+DI+SENNGQNFATA+NLVPLIPVT LP L +SPSDGRK	
Sbjct 181	WKPGDNVSLVSDKFGASPEDIMSENNGQNFATAANNLPVLIPVTRLPLVLARSPSDGRKGG	240
Query 244	IGLPVIGISLGLCTLLVVVSAILLVCVCCCLKMKSINRSASSAETADKLLSGVSGYVSKPT	303
	I LPVIGISLGLCTLLV+ A+LLV V CLKMK+LNRSSAETADKLLSGVSGYVSKPT	
Sbjct 241	IRLPVIGISLGLCTLLVLGLAVLLVYVYCLKMKTINRSASSAETADKLLSGVSGYVSKPT	300
Query 304	MYETGAILEATMNLSEQCKIGESVYKA 330	
	MY T AI+EATMNLSEQCKIGESVYKA	
Sbjct 301	MYGDAIMEATMNLSEQCKIGESVYKA 327	

>dbj|BAG85157.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 513 bits (1320), Expect = 4e-143, Method: Compositional matrix adjust.
Identities = 266/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5	FVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL	63
	F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL	
Sbjct 1	FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL	60
Query 64	TSVSNIFDTSPLSIARASNLOHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSE	123
	T++SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDSE	
Sbjct 61	TNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQGDSE	120
Query 124	YFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHV	183
	YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ IKYLIT+V	
Sbjct 121	YFVATTSYENLTNWRVMDLNPVLSPNKLPPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	180
Query 184	WQPNDNVSFVSNKLGASPDILSENNGQNFATAASNLPVLIPVTLPLDQSPSDGRKHR	243
	W+P DNVS VS+K GASP+DI+SENNGQNFATA+NLVPLIPVT LP L +SPSDGRK	
Sbjct 181	WKPGDNVSLVSDKFGASPEDIMSENNGQNFATAANNLPVLIPVTRLPLVLARSPSDGRKGG	240
Query 244	IGLPVIGISLGLCTLLVVVSAILLVCVCCCLKMKSINRSASSAETADKLLSGVSGYVSKPT	303
	I LPVIGISLGLCTLLV+V A+LLV V CLKMK+LNRSSAETADKLLSGVSGYVSKPT	
Sbjct 241	IRLPVIGISLGLCTLLVLGLAVLLVYVYCLKMKTINRSASSAETADKLLSGVSGYVSKPT	300
Query 304	MYETGAILEATMNLSEQCKIGESVYKA 330	
	MYET AI+EATMNLSEQCKIGESVYKA	
Sbjct 301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>dbj|BAG85176.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 511 bits (1317), Expect = 8e-143, Method: Compositional matrix adjust.
Identities = 265/327 (81%), Positives = 290/327 (88%), Gaps = 1/327 (0%)

Query 5	FVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL	63
	F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL	
Sbjct 1	FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL	60
Query 64	TSVSNIFDTSPLSIARASNLOHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSE	123
	T++SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDSE	
Sbjct 61	TNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQGDSE	120
Query 124	YFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHV	183
	YFVATT Y+NLTNW AV DLNP LS LPIGIQVV PLFCKCPSKNQLD+ IK+LIT+V	
Sbjct 121	YFVATTSYENLTNWRVMDLNPVLSPNKLPPIGIQVVFPLFCKCPSKNQLDKEIKHLITYV	180
Query 184	WQPNDNVSFVSNKLGASPDILSENNGQNFATAASNLPVLIPVTLPLDQSPSDGRKHR	243
	W+P DNVS VS+K GASP+DI+SENNGQNFATA+NLVPLIPVT LP L +SPSDGRK	
Sbjct 181	WKPGDNVSLVSDKFGASPEDIMSENNGQNFATAANNLPVLIPVTRLPLVLARSPSDGRKGG	240
Query 244	IGLPVIGISLGLCTLLVVVSAILLVCVCCCLKMKSINRSASSAETADKLLSGVSGYVSKPT	303
	I LPVIGISLGLCTLLV+V A+LLV V CLKMK+LNRSSAETADKLLSGVSGYVSKPT	
Sbjct 241	IRLPVIGISLGLCTLLVLGLAVLLVYVYCLKMKTINRSASSAETADKLLSGVSGYVSKPT	300
Query 304	MYETGAILEATMNLSEQCKIGESVYKA 330	
	MYET AI+EATMNLSEQCKIGESVYKA	
Sbjct 301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>dbj|BAG85155.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 511 bits (1316), Expect = 1e-142, Method: Compositional matrix adjust.
Identities = 265/327 (81%), Positives = 289/327 (88%), Gaps = 1/327 (0%)

Query 5	FVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL	63
	F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL	
Sbjct 1	FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL	60
Query 64	TSVSNIFDTSPLSIARASNLOHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSE	123

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Sbjct 61 T++SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDSEF 120
TNISNIFDTSPLSIARASNLPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQGDSEF

Query 124 YFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHV 183
YFVAT Y+NLTNW AVMDLNP LS LPIGIQV PLFCKCPSKNQLD+ IKYLIT+V

Sbjct 121 YFVATPSYENLTNWRVMDLNPVLSPNKLPIGIQVEFPLFCKCPSKNQLDKEIKYLITYV 180

Query 184 WQPNNDVSVFVSNKLGASPDILSENNYQNFATAASNLPVLIPVTLPLDLIQSPSDGRKHR 243
W+P DNVS VS+K GASP+DI+SENNYQNFATAA+NLFPVLIPVT LP L +SPSDGRK

Sbjct 181 WKPGDNVSVLSDFKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLFVLARSPSDGRKGG 240

Query 244 IGLPVIIGISLGCTLLVVVSAILLVCCCLMKMSLNRSASSAETADKLLSGVSGYVSKPT 303
I LPVIIGISLGCTLLV+V A+LLV V CLKMK+LNRSASSAETADKLLSGVSGYVSKPT

Sbjct 241 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKT LNRSASSAETADKLLSGVSGYVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
MYET AI+EATMNLSEQCKIGESVYKA

Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

```

>dbj|BAG85163.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 511 bits (1315), Expect = 2e-142, Method: Compositional matrix adjust.
Identities = 265/327 (81%), Positives = 289/327 (88%), Gaps = 1/327 (0%)

```

Query 5 FVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL 63
F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SP SCETYV YI+QSPNFLSL

Sbjct 1 FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDPSFASCETYVPYIAQSPNFLSL 60

Query 64 TSVSNIIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSEF 123
T++SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDSEF

Sbjct 61 TNISNIFDTSPLSIARASNLPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQGDSEF 120

Query 124 YFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHV 183
YFVATT Y+NLTNW AVMDLNP LS LPIGIQV PLFCKCPSKNQLD+ IKYLIT+V

Sbjct 121 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180

Query 184 WQPNNDVSVFVSNKLGASPDILSENNYQNFATAASNLPVLIPVTLPLDLIQSPSDGRKHR 243
W+P DNVS VS+K GASP+DI+SENNYQNFATAA+NLFPVLIPVT LP L +SPSDGRK

Sbjct 181 WKPGDNVSVLSDFKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLFVLARSPSDGRKGG 240

Query 244 IGLPVIIGISLGCTLLVVVSAILLVCCCLMKMSLNRSASSAETADKLLSGVSGYVSKPT 303
I LPVIIGISLGCTLLV+V A+LLV V CLKMK+LNRSASSAETADKLLSGVSGYVSKPT

Sbjct 241 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKT LNRSASSAETADKLLSGVSGYVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
MYET AI+EATMNLSEQCKIGESVYKA

Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

```

>dbj|BAG85154.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 509 bits (1311), Expect = 4e-142, Method: Compositional matrix adjust.
Identities = 264/327 (80%), Positives = 289/327 (88%), Gaps = 1/327 (0%)

```

Query 5 FVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL 63
F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL

Sbjct 1 FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDPSFSCETYVTYIAQSPNFLSL 60

Query 64 TSVSNIIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSEF 123
T++SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDSEF

Sbjct 61 TNISNIFDTSPLSIARASNLPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQGDSEF 120

Query 124 YFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHV 183
YFVATT Y+NLTNW AVMDLNP LS LPIGIQV PLFCKCPSKNQLD+ IKYLIT+V

Sbjct 121 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVFFPLFCKCPSKNQLDKEIKYLITYV 180

Query 184 WQPNNDVSVFVSNKLGASPDILSENNYQNFATAASNLPVLIPVTLPLDLIQSPSDGRKHR 243
W+P D+VS VS+K GASP+DI+SENNY QNFATAA+NLFPVLIPVT LP L +SPSDGRK

Sbjct 181 WKPGDDVSVLSDFKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLFVLARSPSDGRKGG 240

Query 244 IGLPVIIGISLGCTLLVVVSAILLVCCCLMKMSLNRSASSAETADKLLSGVSGYVSKPT 303
I LPVIIGISLGCTLLV+V A+LLV V CLKMK+LNRSASSAETADKLLSGVSGYVSKPT

Sbjct 241 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKT LNRSASSAETADKLLSGVSGYVSKPT 300

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
MYET AI+EATMNLSEQCKIGESVYKA

Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

```

>dbj|BAG85169.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 507 bits (1305), Expect = 2e-141, Method: Compositional matrix adjust.
Identities = 264/327 (80%), Positives = 289/327 (88%), Gaps = 1/327 (0%)

```

Query 5 FVSLTLGAQILYVVMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSL 63
F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVTYI+QSPNFLSL

Sbjct 1 FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDPSFSCETYVTYIAQSPNFLSL 60

Query 64 TSVSNIIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSEF 123
T++SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDSEF

Sbjct 61 TNISNIFDTSPLSIARASNLPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQGDSEF 120

Query 124 YFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHV 183
YFVATT Y+NLTN AVMDLNP LS LPIGIQV PLFC+CPKSNQLD+ IKYLIT+V

Sbjct 121 YFVATTSYENLTNRRVMDLNPVLSPNKLPIGIQVVFPLFCECPKSNQLDKEIKYLITYV 180

Query 184 WQPNNDVSVFVSNKLGASPDILSENNYQNFATAASNLPVLIPVTLPLDLIQSPSDGRKHR 243
W+P DNVS VS+K GASP+DI+SENNYQNFATAA+NLFPVLIPVT LP L +SPSDGRK

Sbjct 181 WKPGDNVSVLSDFKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLFVLARSPSDGRKGG 240

Query 244 IGLPVIIGISLGCTLLVVVSAILLVCCCLMKMSLNRSASSAETADKLLSGVSGYVSKPT 303
I LPVIIGISLGCTLLV+V A+LLV V CLKMK+LNRSASSAETADKLLSGVS YVSKPT

Sbjct 241 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKT LNRSASSAETADKLLSGVSRVYVSKPT 300

```

Query 304 MYETGAILEATMNLSEQCKIGESVYKA 330
 MYET AI+EATMNLSEQCKIGESVYKA
 Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BA085166.1| Nod factor receptor protein [Glycine max]
 Length=327

Score = 501 bits (1291), Expect = 9e-140, Method: Compositional matrix adjust.
 Identities = 260/324 (80%), Positives = 286/324 (88%), Gaps = 1/324 (0%)

Query 5 FVSLTLGAQILYVVLMMFF-TCIEAQSQQTNGTNFSCPSNSPPSCETYVVTYISQSPNFLSL 63
 F L L +QIL +V+M F T I AQSQQ N TNFSCPS+SPPSCETYVVTYI+QSPNFLSL
 Sbjct 1 FPFPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVVTYIAQSPNFLSL 60

Query 64 TSVSNIFDTSPLSIARASNLOHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSE 123
 T++SNIFDTSPLSIARASNL+ +DKL+ QVLL+PVTGCTGNRSFANISYEINQGDSE
 Sbjct 61 TNSINIFDTSPLSIARASNLEPMDDKLVDKQVLLVPVTCGCTGNRSFANISYEINQGDSE 120

Query 124 YFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHV 183
 YFVATT Y+NLTNW AVMDLNP LS LPIGIQVV PLFCKCPSKNQLD+ I+YLIT+V
 Sbjct 121 YFVATTSYENLTNWRVAVMDLNPVLSNKLPIGIQVVFPLFCKCPSKNQLDKIERYLITYV 180

Query 184 WQPNNDNVSVFSNKLGAQPDISENNGYQNFATAASNLPLVLPVTLPLDLIQSPSDGRKHR 243
 W+P DNVS VS+K GASP+DI+SENNGYQNFATA+NLPVLPVTP LP L +SPSDGRK
 Sbjct 181 WKPNDNVSLVSDKFGASPEDIMSENNGYQNFATAANNLPVLPVTRLPVLARSPPSDGRKGG 240

Query 244 IGLPVIIGISLGCTLLVVVSAILLVCVCLMKKSLNRSASSAETADKLLSGVSGYVSKPT 303
 I LPVIIGISLGCTLLV+V A+LLV V CLMKK+LNRSASSAE ADKLLSGVSGYVS+PT
 Sbjct 241 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLMKKTLNRSASSAENADKLLSGVSGYVSRPT 300

Query 304 MYETGAILEATMNLSEQCKIGESV 327
 MYET AI+EATMNLSEQCKIG SV
 Sbjct 301 MYETDAIMEATMNLSEQCKIGISV 324

>emb|CA002936.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 Length=349

Score = 482 bits (1240), Expect = 8e-134, Method: Compositional matrix adjust.
 Identities = 238/351 (67%), Positives = 288/351 (82%), Gaps = 4/351 (1%)

Query 53 YISQSPNFLSLTSSVSNIFDTSPLSIARASNLOHEEDKLIPGQVLLIPVTCGCTGNRSFAN 112
 Y +QSPNFLSL+++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTGCT N SFAN
 Sbjct 1 YRAQSPNFLSLSNISDIFNLSPRIAKASNIEAEDKKLIPDQLLLVPVTCGCTKNHSFAN 60

Query 113 ISYINGQDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQL 172
 I+Y I QGD+E+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCKCPSKNQL
 Sbjct 61 ITYSIKQGDNFFILSITSYQNLTNYLEFKNFNPNSPTLLPLDTRKVSVPFLFCKCPSKNQL 120

Query 173 DRGIKYLITHVWQPNNDNVSVFSNKLGAQPDISENNGYQNFATAASNLPLVLPVTLPLDL 232
 ++GIKYLIT+VWQ NDNV+ VS+K GAS ++L+ENN+ NFTA++N VLIPVT LP L
 Sbjct 121 NKGIKYLITVWQDNNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPTSLPKL 178

Query 233 IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLVCVCLMKKSLNRSASSAETADKL 291
 Q S+GRK L +IIGISLG ++V + LV V CLMKK LNRS SS+ETADKL
 Sbjct 179 DQPSNIGRKRSSSNLALIIGISLGSAFFILVLTLSLVYVYCLMKRLNRSTSSSETADKL 238

Query 292 LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
 LSGVSGYVSKPTMYE AI+E TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
 Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDAEELK 298

Query 352 ILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSLLEWLFSAKSCSETSNS 402
 ILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSLLEWLF++S S+TSNS
 Sbjct 299 ILQKVNHNGLVKLMGVSSDNDGNCFLVVEYAENGSLLEWLFSES-SKTSNS 348

>emb|CA002948.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 Length=337

Score = 465 bits (1197), Expect = 7e-129, Method: Compositional matrix adjust.
 Identities = 228/339 (67%), Positives = 275/339 (81%), Gaps = 3/339 (0%)

Query 48 ETYVVTYISQSPNFLSLTSSVSNIFDTSPLSIARASNLOHEEDKLIPGQVLLIPVTCGCTGN 107
 ETYV Y +QSPNFLSL+++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTGCT N
 Sbjct 1 ETYVAYRAQSPNFLSLSNISDIFNLSPRIAKASNIEAEDKKLIPDQLLLVPVTCGCTKN 60

Query 108 RSFANISYEINQGDSEFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCP 167
 SFANI+Y I QGD+F+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCKCP
 Sbjct 61 HSFANIYTSIKQGDNFFILSITSYQNLTNYLEFKNFNPNSPTLLPLDTRKVSVPFLFCKCP 120

Query 168 SKNQLDRGIKYLITHVWQPNNDNVSVFSNKLGAQPDISENNGYQNFATAASNLPLVLPVT 227
 SKNQL++GIKYLIT+VWQ NDNV+ VS+K GAS ++L+ENN+ NFTA++N VLIPVT
 Sbjct 121 SKNQLNKGIKYLITYVWQDNNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLPVTP 178

Query 228 LLPDLIQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLVCVCLMKKSLNRSASSAE 286
 LP L Q S+GRK L +IIGISLG ++V + LV V CLMKK LNRS SS+E
 Sbjct 179 SLPKLDQSSNIGRKRSSSNLALIIGISLGSAFFILVLTLSLVYVYCLMKRLNRSTSSSE 238

Query 287 TADKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDV 346
 TADKLLSGVSGYVSKPTMYE AI+E T NLS+ CKIGESVYKANI+G+VLAVK+ K+D
 Sbjct 239 TADKLLSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDA 298

Query 347 TEELKILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENG 385
 +EELKILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENG
 Sbjct 299 SEELKILQKVNHNGLVKLMGVSSDNDGNCFLVVEYAENG 337

>emb|CA002942.1| LysM-domain containing receptor-like kinase [Medicago truncatula
 var. truncatula]
 Length=334

Score = 462 bits (1190), Expect = 4e-128, Method: Compositional matrix adjust.
 Identities = 227/336 (67%), Positives = 274/336 (81%), Gaps = 3/336 (0%)

Query 53 YISQSPNFLSLTSSVSNIFDTSPLSIARASNLOHEEDKLIPGQVLLIPVTCGCTGNRSFAN 112


```
Sbjct 1 Y +QSPNFLSL+++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTCGCT N SFAN 60
YRAQSPNFLSLSNISDIFNLSPRIAASNEAEDKKLIPDQLLLVPVTCGCTKNHSFAN
Query 113 ISYEINQGDSEFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQL 172
I+Y I QGD+F+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCKCPSKNQL
Sbjct 61 ITYSIKQGDNFFILSITSYQNLTNYLEFKNFNPNSPTLLPLDTKVSVPFLFCKCPSKNQL 120
DRGIKYLITHVWQPNQDNVSVFVSNKLGASPDILSENNYQGNFTAASNLPLVLIPTLLPDL 232
++G1KYLIT+VWQ NDNV+ VS+K GAS ++L+ENN+ NFTA++N VLIPVT LP L
Sbjct 121 NKG1KYLITYVWQNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPTSLPKL 178
IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLVVCVCLMKMSLNRSASSAETADKL 291
Q S+GRK L +IIGISLG ++V + LV V CLKMK LNRS SS+ETADKL
Sbjct 179 DQPSSNGRKSSSQNLALIIIGISLGAFFILVLTLSLVYVYCLMKRLNRSTSSSETADKL 238
LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
LSGVSGYVSKPTMYE AI+E TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK 298
ILQKVNHNGLVVKLMGVSSDNDGNCFFVVEYAENGSL 387
ILQKVNHNGLVVKLMGVSSDNDGNCFFVVEYAENGSL
Sbjct 299 ILQKVNHNGLVVKLMGVSSDNDGNCFLVVEYAENGSL 334
```

>emb|CA002960.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=333

Score = 458 bits (1179), Expect = 9e-127, Method: Compositional matrix adjust.
Identities = 225/335 (67%), Positives = 272/335 (81%), Gaps = 3/335 (0%)


```
Query 53 YISQSPNFLSLTSSVNFIDTSPLSIARASNLQHEEDKLIPGVLLIPVTCGCTGNRSFAN 112
Y +QSPNFLSL+++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTCGCT N SFAN
Sbjct 1 YRAQSPNFLSLSNISDIFNLSPRIAASNEAEDKKLIPDQLLLVPVTCGCTKNHSFAN 60
Query 113 ISYEINQGDSEFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQL 172
I+Y I QGD+F+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCKCPSKNQL
Sbjct 61 ITYSIKQGDNFFILSITSYQNLTNYLEFKNFNPNSPTLLPLDTKVSVPFLFCKCPSKNQL 120
DRGIKYLITHVWQPNQDNVSVFVSNKLGASPDILSENNYQGNFTAASNLPLVLIPTLLPDL 232
++G1KYLIT+VWQ NDNV+ VS+K GAS ++L+ENN+ NFTA++N VLIPVT LP L
Sbjct 121 NKG1KYLITYVWQNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPTSLPKL 178
IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLVVCVCLMKMSLNRSASSAETADKL 291
Q S+GRK L +IIGISLG ++V + LV V CLKMK LNRS SS+ETADKL
Sbjct 179 DQPSSNGRKSSSQNLALIIIGISLGAFFILVLTLSLVYVYCLMKRLNRSTSSSETADKL 238
LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
LSGVSGYVSKPTMYE AI+E T NLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK 298
ILQKVNHNGLVVKLMGVSSDNDGNCFFVVEYAENGSL 386
ILQKVNHNGLVVKLMGVSSDNDGNCFFVVEYAENGSL
Sbjct 299 ILQKVNHNGLVVKLMGVSSDNDGNCFLVVEYAENGSL 333
```

>gb|AAM19130.1|AC103891_10 Putative protein kinase [Oryza sativa Japonica Group]
gb|ABF94815.1| Protein kinase domain containing protein [Oryza sativa (japonica cultivar-group)]
gb|EAZ26175.1| hypothetical protein OsJ_10042 [Oryza sativa Japonica Group]
Length=624

Score = 426 bits (1095), Expect = 5e-117, Method: Compositional matrix adjust.
Identities = 249/598 (41%), Positives = 357/598 (59%), Gaps = 45/598 (7%)

```
Query 11 GAQILYVVLME-FTCIEAQSQQT-NGTNFSCPSNSPPSCETYTYTISQSPNFLSLTSSVSN 68
G IL VV+ F EA + T F+C ++P C+T+V Y +QSP FL L ++S+
Sbjct 5 GLCILAVVIAFQLAGGEAVTDATARARRFACNVSAP--CDTFVVYRTQSPGFLDLGNISD 62
IFDTSPLSIARASNLQHEEDKLIPGVLLIPVTCGCTGNRSFANISYEINQGDSEFYFVAT 128
+F S IA A+ L E+ L+PGQ LL+PV CGCTG RSFAN++Y I D+F+ +A
Sbjct 63 LFGVSRALIASANKLTETEDGVLLPGQPLLVFVKCGCTGARSFANVTYPIRPRDTFFGLAV 122
TLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHVWQPN 188
T ++NLT++ V +LNP L ++V+PLFC+CP++ +L G + L+T+VWQF D
Sbjct 123 TAFENLTFDFVLVEELNPAEATRLEPWQEVVVLFCRCPTREELSAGSRLLVTVYVWQPGD 182
NVSVFVSNKLGASPDILSENNYQGNFTAASNLPLVLIPTLLPDL-----IQSPSDGRK 241
+VS VS + AS +I + N N T A+ PVLIPV+ P I + K
Sbjct 183 DVSVVSAALMNASAAANIAASNGVAGNSTFATGQPVLI PVSQPPRPFPPLTYGAIADPGAGK 242
HRIGLPVIGISLGCTLLVVVSAILLVVCVCLKM-----KSLNRSAS 283
HR G +I+ S+ + V A+L + + KSLNR S
Sbjct 243 HRRG--IIVATSIAGSF--VACAVLCTAILAYRRYRKAPVPKHVSPKLSWTKSLNRFDS 298
SAETA-----DKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVL 337
++ A DKLL+ VS ++ KP ++ I+EATMNL EQCK+G S Y+AN+E +V
Sbjct 299 NSSIARMINGGDKLLTSVSVQFIDKPIIFREEEIMEATMNLDEQCKLGSSYYRANLEREVF 358
AVKRFKEDVTEELKILQKVNHNGLVVKLMGVSSDNDGN-CFVVEYAENGSLLEEWLFKASC 396
AVK K +V EL+++Q VNH NL KL G+S DG+ F+VYE+AE GSL++WL+ K
Sbjct 359 AVKPAKGNVAGELRMQMNVNHLTKLAGISIGADGDYAFVLVYFAEKGSLDKWLYQKPP 418
SETSNSR--TSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIA 454
+S +L+W QR+ IA+DV+ GL Y+HEH P +VH D+ + NILL + F+AK++
Sbjct 419 CSQPSSSSVATLWDQRLGIALDVANGLLYLHEHTQPSMVHGDVRARNILLTAGFRAKLS 478
NFSMAR--TFTNPMMSKIDVFAFGVVLIELLTGRKAMTTKENGEVVMWLDIWKIFDQ-E 511
NFS+A+ + DVFAFG++L+ELL+GR+A+ + E+ ML +I + D
Sbjct 479 NFSLAKPAAMVDAATSSDVFAFGLLLLELLSGRRRAVEARVGEIGMLRTEIRTVLDAGG 538
ENREERLRKWMDPKLDNYYPIDYALSASLAVNCTADKSLSRPTIAEIVLSLSLLTQP 569
+ R +LRKWMDF L Y +D ALSLA +A CT + + RP +AEI SLS+L QP
Sbjct 539 DKRAAKLRKWMDFTLGGEYGVDAALSLAGMARCTEEDAARRPKMAEIAFSLSVLGQP 596
```

>ref|XP_002468236.1|  hypothetical protein SORBIDRAFT_01g042230 [Sorghum bicolor]

gb|EER95234.1|  hypothetical protein SORBIDRAFT_01g042230 [Sorghum bicolor]
Length=631

GENE ID: 8085264 SORBIDRAFT_01g042230 | hypothetical protein [Sorghum bicolor]
(10 or fewer PubMed links)

Score = 426 bits (1094), Expect = 5e-117, Method: Compositional matrix adjust.
Identities = 245/592 (41%), Positives = 350/592 (59%), Gaps = 56/592 (9%)

```
Query 28  QSQQTNGTNTFSCP-----SNSPPSCETYVTYISQSPNFLSLTSVSNIFDTSPLSIARA 80
      Q+  + TN++ P      S+SPP C+TYV Y +QSP + L S+S++F TS   IA A
Sbjct 18  QAGAQDNTNYTVPAQFACNVSSSPPCDTYVVYRTQSPGYQDLGSIIDLFGTSQARIASA 77

Query 81  SNLQHEEDKLIPGQVLLIPVT-CGCTGNRSFANISYEINQGDSFYFVATTLYQNLTNWHA 139
      + L E+ L PGQ LL+PV+ CGCTG SFAN++Y I QGD+F+ +A Y+NLT +
Sbjct 78  NGLSSEDGVLQPGQPLLVFVSKCGCTGGWSFANVTYPIRQGDTFNLRVSYENLTLYQL 137

Query 140  VMDLNPGLSQFTLPIGIVVPLFCCKPSKNQLDRGIKYLITHVWQPNDNVSFVSNKLG 199
      + +LNP +L +G +V +PLFC+CP+ + IT+VWQ D +S VS +
Sbjct 138  IQNLNPRSPVPTSLQVGQEVTVPLFCRCPPAPAERSS----FITVWQAGDTMSQVSKLMNT 193

Query 200  SPQDILSENNGQNFTAAS--NLFVLIPVTLPLD-----IQSPSDGRKHRIGLPIVIGI 252
      + +I NN + +AS P+LIPV P L S DG+ VIIG
Sbjct 194  TEDEIAEANNVTSSASASLVGQPMILIPVQQRPLPLPHYAAAGDGKSRWRRRAVIIGA 253

Query 253  SLGCTLLVVVSAILLVVCCLK-----MKSLNRSASSAE----- 286
      S+ + VV A L V + L+ M+ +R A + +
Sbjct 254  SVSGS--VVALAALFVAILALRRYRKPSMRLGSRFAVNTKLTWSRNQFGHDSNSNFAHM 311

Query 287  ---TADKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFK 343
      KLL+GVS ++ KP ++ I+EATMNL E+CKIG + Y+A ++G+V AVK K
Sbjct 312  MKLKGKLLTGVSEFIDKPIIFLEEEIMEATMNLDERCKIGSTYYRAKLDGEVFAVKPAK 371

Query 344  EDVTEELKILQKVNHNGLVLMGVSSDNDGN-CFVVVEYAENGSLLEEWLFAKSCSETSNS 402
      DV+ ELK++Q VNH NL+KL G+S DG+ F+VYE+AE GSL++WL+ K S +S
Sbjct 372  GDVSAELKMMQMVNHNANLIKLAGISIGTDGDYAFVLVEFAEKGS�DKWLYQKPPSALPSS 431

Query 403  R---TSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSM 458
      +L+W QR+ SIA+DV+ GL YMHEH P +VH DI + NILL + F+ KI+ FS+
Sbjct 432  SCCTVATLWSGRLSIALDVANGLLYMHEHTQPSMVHGDIRARNILLTAEFRTKISGFSL 491

Query 459  AR-TFTNPMMSKIDVFAFGVVLIELLTGRKAMTTKENGVEVVMWLDIWKIFDQEENREER 517
      A+ + + DVFAFG++L+ELL+GR+AM + E+ MLW++I + D + RE +
Sbjct 492  AKPATAAATSSDVFAFGLLLLELLSGRRAMEARVGSEIGMLWREIRGVLDAGDKREAK 551

Query 518  LRKWMDPKLDNYPIDYALSASLAVNCTADKSLSRPTIAEIVLSLSLLTQP 569
      L KWMDP L + Y +D ALSLA +A CT D + RP + E+V SLS+L QP
Sbjct 552  LGKWMDPALGSEYHMDAALSAGMARACTEDDAARRPNMTEVVFSLSVLVQP 603
```

>gb|EAY89155.1| hypothetical protein OsI_10648 [Oryza sativa Indica Group]
Length=624

Score = 424 bits (1090), Expect = 2e-116, Method: Compositional matrix adjust.
Identities = 248/598 (41%), Positives = 357/598 (59%), Gaps = 45/598 (7%)

```
Query 11  GAQILYVVLMF-FTCIEAQSQT-NGTNFSCPSNSPPSCETYVTYISQSPNFLSLTSVSN 68
      G IL VV+ F +A + T F+C ++P C+T+V Y +QSP FL L ++S+
Sbjct 5  GLCILAIVAFQVTLAGGQAVTDATARARRFACNVSA--CDTFVYVRTQSPGFLDLGNISD 62

Query 69  IFDTSPLSIARASNQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSFYFVAT 128
      +F S IA A L E+ L+PGQ LL+PV CGCTG RSFAN++Y I D+F+ +A
Sbjct 63  LFGVSRALIASANKLTEDGVLLPGQPLLVFVSKCGCTGARSFANVTYPIRPRDTFFGLAV 122

Query 129  TLYQNLTNWHAVMMDLNPGLSQFTLPIGIVVPLFCCKPSKNQLDRGIKYLITHVWQPN 188
      T ++NLT++ V +LNP L +VV+PLFC+CP++ +L G + L+T+VWQ P D
Sbjct 123  TAFENLTDVFLVEELNPAAEATRLPEWQEVVVPLFCRCPTREELSAGSRLLVTVVWQPGD 182

Query 189  NVSFVSNKLGASPDILSENNGQNFTAASNLFVLIPVTLPLD-----IQSPSDGRK 241
      +VS VS + AS +I + N N T A+ PVLIPV+ P I + K
Sbjct 183  DVSVVSAALMNASANAASNGVAGNSTFATGQPVLIIPVSQPPRFPPLTYGAIAADPGAGK 242

Query 242  HRIGLPIVIGISLGTLLVVVSAILLVVCCLK-----MKSLNRSAS 283
      HR G +I+ S+ + V A+L + + KSLNR S
Sbjct 243  HRHG--IIVATSIAGSF--VACAVLCTAILAYRRYRKAPVPKHVSPKLSWTKSLNRFDS 298

Query 284  SAETA-----DKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVL 337
      ++ A DKLL+ VS ++ KP ++ I+EATMNL EQCK+G S Y+AN+E +V
Sbjct 299  NSSIARMINGGDKLLTSVSQFIDKPIIFREEEIMEATMNLDEQCKLGSSYYRANLEREVF 358

Query 338  AVKRFKEDVTEELKILQKVNHNGLVLMGVSSDNDGN-CFVVVEYAENGSLLEEWLFAKSC 396
      AVK K +V EL+++Q VNH NL KL G+S DG+ F+VYE+AE GSL++WL+ K
Sbjct 359  AVKPAKGNVAGELRMMQMVNHNANLTKLAGISIGADGDYAFVLVEFAEKGS�DKWLYQKPP 418

Query 397  SETSNR--TSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIA 454
      +S +L+W QR+ IA+DV+ GL Y+HEH P +VH D+ + NILL + F+AK++
Sbjct 419  CSQPSSSSVATLSWDQRLGIALDVANGLLYLHEHTQPSMVHGDVARNILLTAGFRAKLS 478

Query 455  NFSMAR--TFTNPMMSKIDVFAFGVVLIELLTGRKAMTTKENGVEVVMWLDIWKIFDQ-E 511
      NFS+A+ + + DVFAFG++L+ELL+GR+A+ + E+ ML +I + D
Sbjct 479  NFSLAKPAATVDAATSSDVFAFGLLLLELLSGRRAVEARVGVEIGMLRTEIRTVLDAGG 538

Query 512  ENREERLRKWMDPKLDNYPIDYALSASLAVNCTADKSLSRPTIAEIVLSLSLLTQP 569
      + R +LRKWMDP L Y +D ALSLA +A CT + + RP +AEI SLS+L QP
Sbjct 539  DKRAAKLRKWMDPDPTLGGEYGVDAALSAGMARACTEEDAARRPKMAEIAFSLSVLGQP 596
```

>emb|CA002953.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
Length=313

Score = 417 bits (1071), Expect = 3e-114, Method: Compositional matrix adjust.
Identities = 206/315 (65%), Positives = 252/315 (80%), Gaps = 3/315 (0%)

```
Query 53  YISQSPNFLSLTSVSNIFDTSPLSIARASNQHEEDKLIPGQVLLIPVTCGCTGNRSFAN 112
      Y +QSPNFLSL+++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTCGCT N SFAN
Sbjct 1  YRAQSPNFLSLSNISDQFNLSPLRIAKASNIEADKKLIPDQLLLVVPTCGCTRNHSFAN 60
```

```

Query 113 ISYEINQGDSEFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIVVPIPLFCCKCPSKNQL 172
I+Y I QGD+E+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCCKCPSKNQL
Sbjct 61 ITYSIKQGDNEFFILSITSYQNLTNYLEFKNFENPNLSPTLLPLDTKVSVPPLFCCKCPSKNQL 120

Query 173 DRGIKYLITHVWQPNQDNVSVFNKLGASPDILSENNYQGNFTAASNLPLVLIPTLLPDL 232
++G1KYLIT+VWQ NDNV+ VS+K GAS ++L+ENN+ NFTA++N VLIPT LP L
Sbjct 121 NKG1KYLITYVWQDNQDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPTSLPKL 178

Query 233 IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLVVCVCLMKKSLNRSASSAETADKL 291
Q S+GRK L +IIGISLG ++V + LV V CLMKK LNRS SS+ETADKL
Sbjct 179 DQPSNNGRKSSSQNLALIIGISLGSAFFILVLTLSLVYVYCLMKRLNRSSTSSSETADKL 238

Query 292 LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
LSGVSGYVSKPTMYE AI+E T NLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK 298

Query 352 ILQKVNHNGLVVKLMG 366
ILQKVNHNGLVVKLMG
Sbjct 299 ILQKVNHNGLVVKLMG 313

```

>emb|CA002964.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
 emb|CA002968.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
 Length=311

Score = 414 bits (1065), Expect = 1e-113, Method: Compositional matrix adjust.
 Identities = 205/313 (65%), Positives = 251/313 (80%), Gaps = 3/313 (0%)

```

Query 53 YISQSPNFLSLTSSVSNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCTGNRSFAN 112
Y +QSPNFLSL+++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTGCT N SFAN
Sbjct 1 YRAQSPNFLSLSNISDIFNLSPLRIAKASNIEADKKLIPDQLLLVPVTCGCTKNHSFAN 60

Query 113 ISYEINQGDSEFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIVVPIPLFCCKCPSKNQL 172
I+Y I QGD+E+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCCKCPSKNQL
Sbjct 61 ITYSIKQGDNEFFILSITSYQNLTNYLEFKNFENPNLSPTLLPLDTKVSVPPLFCCKCPSKNQL 120

Query 173 DRGIKYLITHVWQPNQDNVSVFNKLGASPDILSENNYQGNFTAASNLPLVLIPTLLPDL 232
++G1KYLIT+VWQ NDNV+ VS+K GAS ++L+ENN+ NFTA++N VLIPT LP L
Sbjct 121 NKG1KYLITYVWQDNQDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPTSLPKL 178

Query 233 IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLVVCVCLMKKSLNRSASSAETADKL 291
Q S+GRK L +IIGISLG ++V + LV V CLMKK LNRS SS+ETADKL
Sbjct 179 DQPSNNGRKSSSQNLALIIGISLGSAFFILVLTLSLVYVYCLMKRLNRSSTSSSETADKL 238

Query 292 LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
LSGVSGYVSKPTMYE AI+E TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK 298

Query 352 ILQKVNHNGLVVKL 364
ILQKVNHNGLVVKL
Sbjct 299 ILQKVNHNGLVVKL 311

```

>emb|CA002944.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
 Length=307

Score = 408 bits (1049), Expect = 1e-111, Method: Compositional matrix adjust.
 Identities = 201/309 (65%), Positives = 247/309 (79%), Gaps = 3/309 (0%)

```

Query 53 YISQSPNFLSLTSSVSNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCTGNRSFAN 112
Y +QSPNFLSL+++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTGCT N SFAN
Sbjct 1 YRAQSPNFLSLSNISDIFNLSPLRIAKASNIEADKKLIPDQLLLVPVTCGCTKNHSFAN 60

Query 113 ISYEINQGDSEFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIVVPIPLFCCKCPSKNQL 172
I+Y I QGD+E+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCCKCPSKNQL
Sbjct 61 ITYSIKQGDNEFFILSITSYQNLTNYLEFKNFENPNLSPTLLPLDTKVSVPPLFCCKCPSKNQL 120

Query 173 DRGIKYLITHVWQPNQDNVSVFNKLGASPDILSENNYQGNFTAASNLPLVLIPTLLPDL 232
++G1KYLIT+VWQ NDNV+ VS+K GAS ++L+ENN+ NFTA++N VLIPT LP L
Sbjct 121 NKG1KYLITYVWQDNQDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPTSLPKL 178

Query 233 IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLVVCVCLMKKSLNRSASSAETADKL 291
Q S+GRK L +IIGISLG ++V + LV V CLMKK LNRS SS+ETADKL
Sbjct 179 DQPSNNGRKSSSQNLALIIGISLGSAFFILVLTLSLVYVYCLMKRLNRSSTSSSETADKL 238

Query 292 LSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
LSGVSGYVSKPTMYE AI+E TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK 298

Query 352 ILQKVNHN 360
ILQKVNHN
Sbjct 299 ILQKVNHN 307

```

>emb|CA002946.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
 Length=305

Score = 404 bits (1037), Expect = 2e-110, Method: Compositional matrix adjust.
 Identities = 199/307 (64%), Positives = 245/307 (79%), Gaps = 3/307 (0%)

```

Query 53 YISQSPNFLSLTSSVSNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCTGNRSFAN 112
Y +QSPNFLSL+++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTGCT N SFAN
Sbjct 1 YRAQSPNFLSLSNISDIFNLSPLRIAKASNIEADKKLIPDQLLLVPVTCGCTKNHSFAN 60

Query 113 ISYEINQGDSEFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIVVPIPLFCCKCPSKNQL 172
I+Y I QGD+E+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCCKCPSKNQL
Sbjct 61 ITYSIKQGDNEFFILSITSYQNLTNYLEFKNFENPNLSPTLLPLDTKVSVPPLFCCKCPSKNQL 120

Query 173 DRGIKYLITHVWQPNQDNVSVFNKLGASPDILSENNYQGNFTAASNLPLVLIPTLLPDL 232
++G1KYLIT+VWQ NDNV+ VS+K GAS ++L+ENN+ NFTA++N VLIPT LP L
Sbjct 121 NKG1KYLITYVWQDNQDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPTSLPKL 178

Query 233 IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLVVCVCLMKKSLNRSASSAETADKL 291

```

```
Sbjct 179      Q S+GRK      L +IIGISLG      ++V + LV V CLKMK LNRS SS+ETADKL 238
DQPSNNGRKSSSQNLALIIIGISLGAFFILVLTLSLVVYVCLMKRLNLRSTSSSETADKL

Query 292      LSGVSGVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
LSGVSGVSKPTMYE AI+E TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK

Sbjct 239      LSGVSGVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDAEELK 298

Query 352      ILQKVN 358
ILQKVN

Sbjct 299      ILQKVN 305
```

>emb|CA002962.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=304

Score = 400 bits (1028), Expect = 3e-109, Method: Compositional matrix adjust.
Identities = 198/306 (64%), Positives = 244/306 (79%), Gaps = 3/306 (0%)

```
Query 53      YISQSPNFLSLTSSVSNIFDTSPLSIARASNQHEEDKLIPGVLLIPVTCGCTGNRSFAN 112
Y +QSPNFLSL+++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTGCT N SFAN

Sbjct 1        YRAQSPNFLSLSNISDIFNLSPRIAKASNIEAEDKKLIPDQLLLVPVTCGCTKNHSFAN 60

Query 113     ISYEINQGDSEFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQL 172
I+Y I QGD+F+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCKCPSKNQL

Sbjct 61      ITYSIKQGDNFFILSITSYQNLTNYLEFKNFNPNLSPTLLPLDTKVSVPFLFCKCPSKNQL 120

Query 173     DRGIKYLITHVWQPNNDNVSVFVSNKLGASPDILSENNGQNFATAASNLPLVLIPTLLPDL 232
++GIKYLIT+VWQ NDNV+ VS+K GAS ++L+ENN+ NFTA++N VLIPVT LP L

Sbjct 121     NKGIKYLITYVWQNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPVTSLPKL 178

Query 233     IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLVCVCCLMKMSLNRSASSAETADKL 291
Q S+GRK L +IIGISLG ++V + LV V CLKMK LNRS SS+ETADKL

Sbjct 179     DQPSNNGRKSSSQNLALIIIGISLGAFFILVLTLSLVVYVCLMKRLNLRSTSSSETADKL 238

Query 292     LSGVSGVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 351
LSGVSGVSKPTMYE AI+E TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK

Sbjct 239     LSGVSGVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDAEELK 298

Query 352     ILQKVN 357
ILQKVN

Sbjct 299     ILQKVN 304
```

>ref|XP_002517029.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]

gb|EEF45192.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]
Length=615

GENE ID: 8280185 RCOM_0909430 | serine-threonine protein kinase, plant-type, putative [Ricinus communis]

Score = 356 bits (913), Expect = 6e-96, Method: Compositional matrix adjust.
Identities = 221/584 (37%), Positives = 321/584 (54%), Gaps = 72/584 (12%)

```
Query 32      TNGTNFSCPSNSPPSCETYTYIISQSPNFLSLTSSVSNIFDTSPLSIARASNQHEEDKLI 91
T+G + S P C+TY Y + +PNFL L SV ++F S L I+ SN+ LI

Sbjct 30      TDGITCTVNQTSNP-CQTYAFYRAMAPNFLDLASVGLFSVSRMISEPSNIISSPSSPLI 88

Query 92      PGQVLLIPVTCGC-----TGNRSFANISYEINQGDSEFYFVATTLYQNLTNWHAVMDLNP 146
P Q L +P++C C T N S+AN+SY I + D+EY V+TT +QNLT + AV +NP

Sbjct 89      PNQSLFVPISCSRAINSTTNLSYANLSYTIKKDDTFYLVSTTQFQNLTTYQAVQVVNPT 148

Query 147     LSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHVWQPNNDNVSVFVSNKLGASPDILS 206
L L IG +V+ P+FCCKP++ QL + ++I++V+QP+DN+S V++ G + Q I+

Sbjct 149     LVPITLLEIGQEVFPFVFCCKPNQTLQVQVNFMSYVFPQSDNLSLVASSFGTNTQSIVD 208

Query 207     ENNYGQNFATAASNLPLVLIPTLLPDLIQ-----SPSDGRKHRIGLPVIIGISLG-CTLLV 260
N GN + +PV LP L Q S +K R GL + + LG C L+

Sbjct 209     VN--GNIIQPFDT--IFVPVNRPLPQLSQPVVVSVPTEKKERKGLITGLAVGLGVCGLL 264

Query 261     VVSAILLVCVCCLMKMSLNRSASS-----AETADKLLSGVSGVSKPT 303
IL++ + LNR S E KL++ VS + K

Sbjct 265     ----ILIGSVWFREGKLNRRKKEEDEDKKRLRFYKGEKGLTETMETKLIADVSDCLDKYR 320

Query 304     MYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHNGLVK 363
+++ + EAT +E I SVYK +I G+ A+K+ K + EELKILQKVNHNGLVK

Sbjct 321     VFKIDELKEATDGFENENFLIQGSVYKGSINGQDYAIKKMKWNAYEELKILQKVNHNGLVK 380

Query 364     LMGVSSDN-DGNCFFVVEYAENGSLLEEWLFAKSCSETSNRSRTSLTWCQRISIAVDVSMGL 422
L G D+ DG+C+++YEY ENGL WL N L W R+ IA+DV+ GL

Sbjct 381     LEGFCIDSEDGSCYLIYEYIENGSLHSLWLI-----NKNEKLNWKTRLRIADVANG 433

Query 423     QYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMM----- 467
QY+HEH PR+VH+DI SSNILLDS +AKIANF +A++ N +

Sbjct 434     QYTHEHTRPRVVRHDKIKSSNILLDSTMRKIANFGLAKSGCNAITMHIVGTQGYIAPEYL 493

Query 468     -----SKIDVFAFGVVLIELLTGRKAMTTKENGVEVVMLWKDIWKIFD-QEENREERLRK 520
+++ +DV+ +FGVVL+EL+G++A+ E G V LW + +D EE + +RL+

Sbjct 494     TDGVVSTRMDVFSFGVVLLELISGKEAI--DEEGRV--LWAKVSGNWDGNEEKVKRLKG 549

Query 521     WMDPK-LDNYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSL 563
+MD L ++ + + ++AV C RP++ +IV L

Sbjct 550     FMDESLLRESCSMESIIVMNVAVACLHKDPAKRPSMVDIVYDL 593
```

>ref|XP_002280070.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length=622

GENE ID: 100264758 LOC100264758 | hypothetical protein LOC100264758 [Vitis vinifera]

Score = 348 bits (893), Expect = 1e-93, Method: Compositional matrix adjust.
Identities = 214/590 (36%), Positives = 329/590 (55%), Gaps = 70/590 (11%)

```

Query 27  AQSQ-QTNGTNFSCPSN-SPSPCETIYVTIYSQSPNFLSLTSVSNIFDTSPLSIARASNLO 84
          +Q+Q + N T + C +N S   C T+  Y + SPNFL L S+ ++F S L I+ SN+
Sbjct 27  SQAQPEPNATGYPCSANLSSYPCHTFAFYTATSPNFLDLASIGDLFWVSRMISEPSNIS 86

Query 85  HEEDKLIPGQVLLIPVTCGC-----TGNRSFANISYEINQGDSEFYFVATTLYQNLTNWHA 139
          + L+ GQ L +P+ C C   T   S+AN+SY I  GD+FY V+T  + NLT +++
Sbjct 87  SPSNPLVAGQSLFVPLNCSCNSVNTTTAISYANLSYTIKSGDTFYLVSTFSFLNLTYYYS 146

Query 140  VMDLNPGLSQFTLPPIGQVVIPLFCKCPSKNQLDRGIKYLITHVWQPNDNVSFVSNKLGA 199
          V  +NP L   L +G +V+ P+PCKCP++ Q L  G+ +LI++V+QP+DN++ V+  LG+
Sbjct 147  VEIVNPTLVPTDLDVGDVKVIFPIFCKCPNETQLRNGVNFILISYVFQPSDNLTGVAASLGS 206

Query 200  SPQDILSENNGYQNFTAASNLPVLIPVTLIPDLIQ-----SPSDGRKHRIGLPVIIGI 252
          I+  N  G N   + +PV+ LP++ Q   + S +  R G  VIIG+
Sbjct 207  DTASIIDVN--GDNIQPFQT--IFVPVSRLPNISQPNVTASVATSVRKVERKG--VIIGL 260

Query 253  SLG---CTLLVV--VSAILLVCCVCLMKMSL-----NRSASSAETADKLLSGVSGY 298
          ++G  C +L+V  +  + V  K+K +   R   L++ VS
Sbjct 261  AIGLGVCGIILLVLLIGVWVYRHVMVEKIKEIEGDKERPLVGRGTGLKAEENVLMADVSDC 320

Query 299  VSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNH 358
          + K +Y   + +AT  SE+  I  SVYK +I+G++ A+K+ K +  EELKILQKVNH
Sbjct 321  LDYKVKVYGIEELRDATGGFSESLIQSGSVYKSIDGELYAIKKMKWNAYEELKILQKVNH 380

Query 359  GNLVKLMGVSSD-NDGNCFFVVEYAENGSLLEEWLFAKSCSETSNSRTSLTWCQRISIAVD 417
          GNLV+L G  D  D  C++VYE+ ENGL+ WL   +  L W  R+ IA+D
Sbjct 381  GNLVRLEGFCIDPEDATCYLVYEFVENGSLQSWLHG-----DRDEKLNWKNRLRIAID 433

Query 418  VSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPM----- 467
          V+  GLQY+HEH  PR+VH+DI  SSNILLD N +AKIANF +A++ N +
Sbjct 434  VANGLYIHEHTRPRVVKHDIKSSNILLDGNMRAKIANFGLAKSGCNAITMHIVGTQGYI 493

Query 468  -----SKIDVFAFGVVLIELLTGRKAMTTKENGVEVVMWKDIWKIFD--QEENR 514
          +++DVE+FGVVL+EL++G++A+  E G V  LW  I +  E+ +
Sbjct 494  APEYLADGVVSTRMDFVSFGVVLLELISGKEAV--DEEGRV--LWMSARGILEGKDEKVK 549

Query 515  EERLRKWMDDPK-LDNYYPIDYALSASLAVNCTADKLSRPTIAEIVLSL 563
          +R++ WMD  L  +D  +++ ++A  CT  RP++ +IV +L
Sbjct 550  AKRVKDWMDLEGLRESCMDSVINVMATACTHRDPSKRPSMVDIVYAL 599

```

>emb|CB126350.3| unnamed protein product [Vitis vinifera]
Length=595

Score = 343 bits (881), Expect = 3e-92, Method: Compositional matrix adjust.
Identities = 212/576 (36%), Positives = 324/576 (56%), Gaps = 69/576 (11%)

```

Query 27  AQSQ-QTNGTNFSCPSN-SPSPCETIYVTIYSQSPNFLSLTSVSNIFDTSPLSIARASNLO 84
          +Q+Q + N T + C +N S   C T+  Y + SPNFL L S+ ++F S L I+ SN+
Sbjct 27  SQAQPEPNATGYPCSANLSSYPCHTFAFYTATSPNFLDLASIGDLFWVSRMISEPSNIS 86

Query 85  HEEDKLIPGQVLLIPVTCGC-----TGNRSFANISYEINQGDSEFYFVATTLYQNLTNWHA 139
          + L+ GQ L +P+ C C   T   S+AN+SY I  GD+FY V+T  + NLT +++
Sbjct 87  SPSNPLVAGQSLFVPLNCSCNSVNTTTAISYANLSYTIKSGDTFYLVSTFSFLNLTYYYS 146

Query 140  VMDLNPGLSQFTLPPIGQVVIPLFCKCPSKNQLDRGIKYLITHVWQPNDNVSFVSNKLGA 199
          V  +NP L   L +G +V+ P+PCKCP++ Q L  G+ +LI++V+QP+DN++ V+  LG+
Sbjct 147  VEIVNPTLVPTDLDVGDVKVIFPIFCKCPNETQLRNGVNFILISYVFQPSDNLTGVAASLGS 206

Query 200  SPQDILSENNGYQNFTAASNLPVLIPVTLIPDLIQ-----SPSDGRKHRIGLPVIIGI 252
          I+  N  G N   + +PV+ LP++ Q   + S +  R G  VIIG+
Sbjct 207  DTASIIDVN--GDNIQPFQT--IFVPVSRLPNISQPNVTASVATSVRKVERKG--VIIGL 260

Query 253  SLGCTLLVVVSAILLVCCVCLMKMSLNRSASSAETADKLLSGVSGYVSKPTMYETGAILE 312
          ++G  L   L+  LK + +N   L++ VS  + K  +Y  + +
Sbjct 261  AIG--LGGDKERPLVGRGTGLKAEVN-----LMADVSDCLDKYKVYGIEELRD 307

Query 313  ATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHNGLVKLMGVSSD-N 371
          AT  SE+  I  SVYK +I+G++ A+K+ K +  EELKILQKVNHNGLV+L G  D
Sbjct 308  ATGGFSESLIQSGSVYKSIDGELYAIKKMKWNAYEELKILQKVNHNGLVLRLEGFCIDPE 367

Query 372  DGNCFFVVEYAENGSLLEEWLFAKSCSETSNSRTSLTWCQRISIAVDVSMGLQYMHEHAYP 431
          D  C++VYE+ ENGL+ WL   +  L W  R+ IA+DV+ GLQY+HEH  P
Sbjct 368  DATCYLVYEFVENGSLQSWLHG-----DRDEKLNWKNRLRIAIDVANGLYIHEHTRP 420

Query 432  RIVHRDITSSNILLDSNFKAKIANFSMARTFTNPM-----SKI 470
          R+VH+DI  SSNILLD N +AKIANF +A++ N +  +++
Sbjct 421  RVVHKDKIKSSNILLDGNMRAKIANFGLAKSGCNAITMHIVGTQGYIAPEYLADGVVSTRM 480

Query 471  DVFAFGVVLIELLTGRKAMTTKENGVEVVMWKDIWKIFD--QEENREERLRKWMDDPK-LD 527
          DV+FGVVL+EL++G++A+  E G V  LW  I +  E+ + +R++ WMD  L
Sbjct 481  DVFSFGVVLLELISGKEAV--DEEGRV--LWMSARGILEGKDEKVKAKRVKDWMDLEGLLR 536

Query 528  NYYPIDYALSASLAVNCTADKLSRPTIAEIVLSL 563
          +D  +++ ++A  CT  RP++ +IV +L
Sbjct 537  ESCMDSVINVMATACTHRDPSKRPSMVDIVYAL 572

```

>gb|AAT00791.1| SYM10-like protein [Galega orientalis]
Length=244

Score = 336 bits (862), Expect = 4e-90, Method: Compositional matrix adjust.
Identities = 174/244 (71%), Positives = 200/244 (81%), Gaps = 3/244 (1%)

```

Query 222  VLIPVTLIPDLIQSPSDGRKHRIG-LPVIIGISLGCTLLVVVSAILLVCCVCLMKMSLNR 280
          +LIPVT LP L Q  S G   LPVIIGISLG  +VV  + LV V  CLMK LNR
Sbjct 1  ILIPVTNLPLKDQSSSGSISSSKKLPVIIGISLGSAFFIVVLTLSLVVYCYLKMRLNR 60

Query 281  SASSAETADKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVK 340
          S S  AETADKLLSGVSGYVSKPTMYE  I+EAT +LS+QCKIGESVYKANI+  + LAVK
Sbjct 61  STSLAETADKLLSGVSGYVSKPTMYEIDVIMEATNDLSDQCKIGESVYKANIDSRDLAVK 120

Query 341  RFKEDVTEELKILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSLLEEWLFAKSCSETS 400
          + K+D +EELKILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSL++WLF+++ S+TS
Sbjct 121  KIKKDASEELKILQKVNHNGLVKLMGVSSDNDGNCFLVVEYAENGSLDDWLFSEA-SKTS 179

Query 401  NS-RTSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMA 459
          NS  +SLTW  QRI  IA+DV++GLQYMHEH  YPRI+HR  IT+SNIL+DSNFKAKIANF

```

Sbjct 180 NSIVSSLTWSQRIGIAMDVAVGLQYMHEHTYPRIIHYRITTSNILIDSNFKAKIANFLDG 239
 Query 460 RTFT 463
 +T T
 Sbjct 240 KTST 243

>gb|ABR17803.1| unknown [Picea sitchensis]
 Length=536

Score = 333 bits (855), Expect = 3e-89, Method: Compositional matrix adjust.
 Identities = 201/519 (38%), Positives = 282/519 (54%), Gaps = 65/519 (12%)

Query 107 NRSFANISYEINQGDSEYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCCK 166
 N S AN++Y I GD+FY ++T ++NLT + AV NP L L IG IP+ CKC
 Sbjct 3 NYSQANVTYTIYGGDTFYLISTRKFEENLTPPAVEVTNPTLVVTNLQIGSLATIPIRCKC 62

Query 167 PSKNQLDRGIKYLIHVWQPNNDVSVFVSNKLGASPDILSENNGQNFTAASNLPVLIPV 226
 PS Q+ G K LIT+V P D + +S K GA Q++ S N S L L+PV
 Sbjct 63 PSNAQVNTYTKMLITYVVPDGTLLNISQKFGADLQNLKSLNGINSTLIPIYSTL--LVPV 120

Query 227 TLLPDLIQ-----SPSDGRKHRIGLPVIGISLGCTLLVVSAILL 267
 + P L Q + S G H +IG S+G + VV A+L+
 Sbjct 121 SQKEVLAQPPSPSPSPPPPLVVNNATSSGGGLHG---GAVIGASVGGSAAVVCIALLI 177

Query 268 VCVCCLMKMSLNRSASS-----AETADKLLSGVSGYVSKPTMYETGAILEATMN 316
 CV K+S +++ S +T KL++G+S V P MY + +AT N
 Sbjct 178 FCVVIRKRRSYKQTSISEDQRPPSDVGVGKTSKMLTGISDCVENPFMYSIEDLDKATQN 237

Query 317 LSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHNVLKMGVSSDNDGNCF 376
 S C I SVYK ++G+ A+K K D+++ELKILQKVNH NLVKL GV ++G +
 Sbjct 238 FSPCLNIEGVS YKGTLDGRDYAIKLMKGDISQELKILQKVNHTNLVKLEGVCSISSEGSQSY 297

Query 377 VVYEYAENGSLLEWLFKASCSETS-----SRTSLTWCQRISIAVDVSMGLQYMHEHAYPR 432
 +VVEY EN SL WL E + S +SL W R+ +A+DV+ GLQY+HEH P
 Sbjct 298 LVVEYIENSSLNLTWLHDPESVENMSPIGWSSSSLPWKTRQLVALDVANGLQYIHEHTPS 357

Query 433 IVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMS-----KID 471
 +VH+DI SSNILLD NF+AKIANF MA++ N + K+D
 Sbjct 358 VVHKDIKSSNILLDGNFRAKIANFMAKSGINALTKHIMGTQGYMAPEYLDGFVSPKLD 417

Query 472 VFAFGVVLIELLTGRKAMTTKEN---GEVVMWLKDIWKIFDQEEENREERLRKWMDPKLD 527
 VFAFGVVL+E+++G++A+ + G+ +LW I + + E+ E +LRKW+D L
 Sbjct 418 VFAFGVVLLEMSISKEAIVRERGVPLAGKAGLLWTQIRPLEGED-IEGKLRKWVDRNLQ 476

Query 528 NYYPIDYALSLASLAVNCTADKLSRPTIAEIVLSLSLL 566
 N Y +D L +A++A C + ++RPT+ EIV LS L
 Sbjct 477 NAYTMSILGVATIRACVEEDPVARPTLPEIVYKLSNL 515

>emb|CAN66762.1| hypothetical protein [Vitis vinifera]
 Length=591

Score = 328 bits (841), Expect = 1e-87, Method: Compositional matrix adjust.
 Identities = 203/569 (35%), Positives = 312/569 (54%), Gaps = 59/569 (10%)

Query 27 AQSQ-QTNGTNFSCPSN-SPSCETYVTYISQSPNFLSLTSVSNIFDTSPLSIARASNLO 84
 +Q+Q + N T + C +N S C T+ Y + SPNFL L S+ ++F S L I+ SN+
 Sbjct 27 SQAQPEANATGYPCSANLSSYPCHTFAYTATSPNFLDLASIGDLFWVSRMLISEPSNIS 86

Query 85 HEEDKLIPGQVLLIPVTCGC-----TGNRSFANISYEINQGDSEYFVATTLYQNLTNWH 139
 + L+ GQ L +P+ C C T S+AN++Y I GD+FY V+T + NLT +++
 Sbjct 87 SPSPNPLVAGQSLFVPLNCSCNSVNATTAISYANLTYTIKSGDTFYLVSTFSFLNLTYY 146

Query 140 VMDLNPGLSQFTLPIGIQVVIPLFCCKPSKNQLDRGIKYLIHVWQPNNDVSVFVSNKLG 199
 V +NP L L +G +V+ P+PCKCP++ QL G+ +LI++V+QP+DN++ V+ LG+
 Sbjct 147 VEIVNPTLVPTDLVDGDKVIFPIFCCKPNETQLRNGVNFLLISYVFQPSDNLTVGAASLGS 206

Query 200 SPQDILSENNGQNFTAASNLPVLIPVTLTLLPDLIQ-----SPSDG--RKHRIGLPVIGI 252
 I+ N G N + +PV+ LP++ Q SP+ R R G IIG+
 Sbjct 207 DTASIIDVN--GDNIQPFQT--IFVVPVSRLEPNISQPNVTASPATSVRRVERKG--AIIGL 260

Query 253 SLG---CTLLVV--VSAILLCVCCLMKMSL-----NRSASSAETADKLLSGVSGY 298
 S+G C +L+V + + V K+K + R + L+ + VS
 Sbjct 261 SIGLGVCGILLVLLIGVWYRHMVEKIKEIEGDKERPLVGRGSGLKAEVNLMAVDSDC 320


Query 299 VSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVN 358
 + K +Y + +AT SE+ I SVYK +I+G++ A+K+ K + EELKILQKVN
 Sbjct 321 LDKYKYVIGIEELDATGGFSERSLIQGSVYKSIDGELYAIKKMKWNAYEELKILQKVN 380


Query 359 GNLVKLMGVSSD-NDGNCFVVYEYAENGSLLEWLFKASCSETSNSRTSLTWCQRISIAVD 417
 GNLV+L G D D C++VYE+ ENGL+ WL + L W R+ IA+D
 Sbjct 381 GNLVRLLEGFCIDPEDATCYLVYEFVENGSLQSWLHG-----DRDEKLNWKNRLRIAID 433

Query 418 VSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKIDVFAFGV 477
 V+ GLQY+HEH PR+VH+DI SSNILLD N +AKIANF +A++ N
 Sbjct 434 VANGLYIHEHTRPRVVKDIKSSNILLDGNMRAKIANFGLAKSGCN-----A 481

Query 478 VLIPELLTGRKAMTTKENGEMVWLKDIWKIFD--QEEENREERLRKWMDPK-LDNYYPIDY 534
 + + ++ + E G V LW I + E+ + +R++ WMD L +D
 Sbjct 482 ITMHIVGTQGKEAVDEEGRV--LWMSARGILEGKDEKVKAKRVKDWMEGLLRESCSMDS 539

Query 535 ALSLASLAVNCTADKLSRPTIAEIVLSL 563
 +++ ++A CT RP++ +IV +L
 Sbjct 540 VINVMATACTHRDPSKRPSMVDIVYAL 568

>ref|XP_001767824.1|  predicted protein [Physcomitrella patens subsp. patens]

gb|EDQ67338.1|  predicted protein [Physcomitrella patens subsp. patens]
 Length=658

GENE ID: 5931014 PHYPADRAFT_132645 | hypothetical protein
 [Physcomitrella patens subsp. patens] (10 or fewer PubMed links)

Score = 309 bits (791), Expect = 8e-82, Method: Compositional matrix adjust.
 Identities = 218/631 (34%), Positives = 328/631 (51%), Gaps = 98/631 (15%)

```

Query 25 IEAQSQQTNGTNSFCSPNSPPSCETYVTYI---SQSPNFLSLTSVSNIFDTSPLSIARAS 81
Sbjct 24 ISAQQQYRNTSGYTCSGTT---RCQTYAFYRTAGSQS----TLTSIVTLFNTSVEGIATAS 77

Query 82 NLQHEEDKLIP---GQVLLIPVTCGCTGNRSFANISYEINQGDSFYFVATTLYQNLTNWH 138
Sbjct 78 ++ + ++ IP L IP+ C C N A S +I GD+ Y A YQ LT W
DV---DPNRTIFFNDRDPLYIPLNCSCFNNTFRALTSQQIKSGDTMYKFANGTYQGLTTWE 135

Query 139 AVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHVWQPNDNVSVFSNKL 198
Sbjct 136 A+ NP + + +G +VIPL C CP+ Q G + L+T+ P++ + F+S
AISVANPTVIITNMTVGDLVIPLRCACPTTQRRAGSRILLTYSIFPDETLKFISGLFN 195

Query 199 ASPQDILSENNGYQGNFTAAS-----NLPVLIPVTL-----PDLIQSPSDGRKHRIGL 246
Sbjct 196 ++ + NN + A+ LP L+P++ + P +++P G +
IPEVELQTANNGASSANLAFTLLVPLPSLPLSTMKFPPSPPPSVEAP--GPAPSTLV 253

Query 247 FVI-----IGISLGCTLLVVSAILLVCVCLMKMS-----LNR 280
Sbjct 254 FVI IGI G + + A +L CV C +K LNR
FVITNKDPKSTSMYIGIVFGGFGMAL--AFILACVLCATVKRYKNIIRKIEYENRGLLNR 311

Query 281 SAS-----SAETAD-KLLSGVSGYVS---KPTMYETGAILEATMNLSEQCKIGESVYKANI 332
Sbjct 312 +S S +TA+ L+SG++ K T + + AT + SE +I SV+ A+
KSSVTDLDSLDTANSSLSVGMTDLFGCDKLTKFSYEELDTATNHFSEDNRIQGSVFLAKL 371

Query 333 EGKVLAVKRFKEDVTEELKILQKVNHGNNLVKLMGV-SSDNDG---NCFVVVEYAENGSL 388
Sbjct 372 G +A+KR K ++++ELKIL +V+HGN+VKL+G+ + D+DG N ++VVEYAENGSL
NGSFVAIKRMKGNMSDELKILSQVHHGNVVKLVGMCDSDGRSENLYIVVEYAENGSL 431

Query 389 EWLFAKSCSETSNRST---LTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILL 445
Sbjct 432 +L + TSN S L W R+ IAVD++ GL+Y+H + P +VH+D+ SSNILL
DCLHHQMAYPTSNFSSRVGLLIWNTRMQIAVDIASGLELYLHNYTNPSLVHKDVKSSNILL 491


Query 446 DSNFKAKIANFSMARTFTN----PMM-----SKIDVFAFGVVL 479
Sbjct 492 D NF+AK+ANF MA+ + P+M +K DVF+FGVVL
DKNFRKAVNANFGMAKPADSGEPGLMTEHIVGTQGYMAPEYLEHGLVSTKADVFSFGVVL 551

Query 480 IELLTGRKAMTTKENGVEVVMWKDIWKIFDQENREERLRKWMDPKLDNYYPIDYALSLA 539
Sbjct 552 +ELL+GR+A+ GE ML I + ++ + +L+ WMDP+L N YP D ALS+A
LELLSGREAI+CNDDGGGEFTMLSATISNVLSGDD-QMAKLQAWMDPRLQNAYPDIALSVA 610

Query 540 SLAVNCTADKSLSRPTIAEIVLSLSLLTQPS 570
Sbjct 611 LA +C SRP + +I +LS ++ S
ILAKSCVETDPRSRPDMKQISFALSKMSSAS 641

```

>ref|XP_002311653.1|  predicted protein [Populus trichocarpa]

gb|EEE89020.1|  predicted protein [Populus trichocarpa]
Length=524

GENE ID: 7473444 POPTRDRAFT_564909 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score = 308 bits (788), Expect = 2e-81, Method: Compositional matrix adjust.
Identities = 180/500 (36%), Positives = 278/500 (55%), Gaps = 56/500 (11%)

```

Query 109 SFANISYEINQGDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPS 168
Sbjct 13 SANI+Y I G++FY V+T +QNL+ + +V NP L L IG++V+ P+FCCKP
SSANITYTIEAGNTFYIVSTKYFQNLTTYQSVELFNPTLIEPELLDIGVEVIFPIFCCKPH 72

Query 169 KNQLDRGIKYLITHVWQPNDNVSVFSNKLGPQDILSEN-----YQGNFTAASNLPVL 223
Sbjct 73 + QL + YL+++V+Q+P+DN+S V++ G Q I+ N Y F + +LP L
QTQLQNKVNLYVSVFQPSDNLSSVASTFGVETQSIQVDVNGNNIQPYDTIFVVPVNLPLQL 132

Query 224 I-PVTLPLDILQSPSDGRKHRIGLPVIGISLGCTLLVVSAILLVCVCLMKM----- 276
Sbjct 133 P ++P P + + + + +G+ + LLV+VS + LK +
AQPTVVVPSGAPPEKTERKGVII GLAVGLGIAGLLLVLSGVWFYREGVLKKRRDVEKV 192

Query 277 -----SLNRSASSAETAD-KLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYK 329
Sbjct 193 LN + + + L++ VS + K +++ + EAT SE C I SV+K
EEKRRMQLNNGSGKGLKIDVSLMADVSDCLDKYRVFKIDELKEATNGFSENCLIEGSVFK 252

Query 330 ANIEGKVLAVKRFKEDVTEELKILQKVNHGNNLVKLMGVSSD-NDGNCFFVVEYAENGSL 388
Sbjct 253 +I G+ Y A+K+ K + EELKILQKVNHGNNLVKL G D NC++VYE+ ++GSL
GSINGEYTAIKMKMNACEELKILQKVNHGNNLVKLEGFCDPEDANCYLVEYFVDSGSLH 312

Query 389 EWLFAKSCSETSNRSTSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSN 448
Sbjct 313 WL N + L+W R+ +A+DV+ GLQY+HEH PR+VH+DI SSNILLDS+
SWLH-----RNEKEKLSWKTRLRVAIDVANGLYIHEHTRPRVVKDIKSSNILLDS 365

Query 449 FKAKIANFSMARTFTNPM-----SKIDVFAFGVVLIELLTGRK 487
Sbjct 366 +AKIANF +A+T N + +++DVF+EGVVL+EL++GR+
MRKIANFGLAKTGCNAITMHIVGTQGYIAPEYLADGVVSTRMDVFSFGVVLLELISGRE 425

Query 488 AMTTKENGVEVVMWKDIWKIFD---QEENREERLRKWMDPK-LDNYYPIDYALSLASLAV 543
Sbjct 426 A+ E G+V LW + + + +E + +RL WMD L+ ++ ++ ++A+
AI--DEEGKV--LWAEAGVLEGNVEERRKVKRLTAWMDKVLLEESCMESVMNTMAVAI 481

Query 544 NCTADKSLSRPTIAEIVLSL 563
Sbjct 482 C RP++ +IV +L
ACLHRDPSKRPSMVDIYVAL 501

```

>gb|EAY87082.1| hypothetical protein OsI_08480 [Oryza sativa Indica Group]
Length=651

Score = 299 bits (765), Expect = 8e-79, Method: Compositional matrix adjust.
Identities = 196/601 (32%), Positives = 307/601 (51%), Gaps = 85/601 (14%)

```

Query 36 NFSCPSNSPPSCETYVTYISQSPNF-LSLTSVSNIFDTSPLSIARASNLQHEEDKLIPGQ 94
Sbjct 39 F+C +N+ C Y Y + L ++ ++F S +A A+NL L Q
GFNCTANATYPCPAYALYRAGFGGVPLEFAAIGDLFAASRFMVAHANNLSTSA-VLAARQ 97

Query 95 VLLIPVTCGCTGN--RSFANISYEINQGDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTL 152
Sbjct 98 LL+P+ CGC ++A + Y+IN GD+++ V+TT QNLT + AV +NP L L
PLLVPLQCGCPSRSPNAYAPMQYQINAGDTYWIVSTTKLQNLTYQYQAVERNVPTLVPTNL 157

Query 153 PIGIQVVIPLFCKCPSKNQLDRGIKYLITHVWQPNDNVSVFSNKLGPQDILSENNGYQ 212

```

```

Sbjct 158 IG V P+FC+CP+ + L+T+V QP D + ++ Q ++S N Q 214
DIGGIVTFPIFCQCPTA---EDNATALVTYVMQPGDTYASIAATAFAVDAQSLVSLNGPEQ
Query 213 NFTAASNLPVLIPVT-----LLPDLIQ-----SPSDGRKHRIGLPIVII 250
S+ +L+P+ LP +++ +P+ +R G+ +
Sbjct 215 GTRNLSSPEILVPLRRQVPEWLPPIVRVNNISTTPASPPPSNTFAPTIVVSNNRDGVVTGL 274
Query 251 GISLGCTLLVVVSAILLVVCVCLKMKSLNRSASSAETADK----- 290
I LG + + +LL+ ++K+ R A + + D
Sbjct 275 AIGLGVVGGLLWLLQMLLLGLWRRLKARGRRAEAVASGDGEGGRFTKAASGGGGGGGGG 334
Query 291 --LLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTE 348
L+S +S ++ K +++ + T ++ I SVYKA I+G+V AVK+ K D E
Sbjct 335 RFLVSDISEWLDKYKVKFVEELES GTGGFDDEHLIQGSVYKAYIDGVEVFAVKMKWDACE 394
Query 349 ELKILQKVNHNGLVKLMGVSSDND-GNCFVVEYAENGSLLEEWLFAKSCSETSNSRTSLT 407
ELKILQKVNH NLVKL G +++ G+C++VVEY ENGS+ WL + + L
Sbjct 395 ELKILQKVNHNGLVKLEGFCINSETGDCYLVVEYVENGSLDLWLMDR-----DRARRLD 448
Query 408 WCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNP-- 465
W R+ IA+D++ GLQY+HEH +PR+VH+DI SSN+LLD +AKIANF +A+T N
Sbjct 449 WRARLHIALDLAHLGLQYIHEHTWPRVVKDIKSSNVLLDDRMRAKIANFGLAKTGHNAVT 508
Query 466 -----MMSKIDVFAFGVVLIELLTGRKAMTTKENGEVVMWKDI-W 505
+ +K+DVFA+GVVL+EL++GR+A+ + +GE LW D
Sbjct 509 THIVGTQGYIAPEYLADGLVTTKMDVFAYGVVLELVSGREAV-SDDSGE--PLWADADE 565
Query 506 KIFDQENNR-EERLRKWMDPKL-DNYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSL 563
++F E R E R+ WMDP L + P S+ S+A C R P++ ++ +L
Sbjct 566 RLFRGREERLEARVAAMWDPALAEQTCPPGSVASVSVAKACLRDPAKRFSMVDVAYTL 625
Query 564 S 564
Sbjct 626 S 626

```

>emb|CA002950.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=243

Score = 298 bits (762), Expect = 2e-78, Method: Compositional matrix adjust.
Identities = 150/245 (61%), Positives = 189/245 (77%), Gaps = 3/245 (1%)

```

Query 53 YISQSPNFLSLTSSVNI FDTSPLSIARASNLOHEEDKLIPGQVLLIPVTCGCTGNRSFAN 112
+QSPNFLSL+++S+IF+ SPL IA+ASN++ E+ KLIP Q+LL+PVTGCT N SFAN
Sbjct 1 YRAQSPNFLSLSNISDIFNLSPRIAKASNIEADKKLIPDQLLLVPVTCGCTKNHSFAN 60
Query 113 ISYINGGDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIVVPLFCCKPSKNQL 172
I+Y I QGD+E+ ++ T YQNLTN+ + NP LS LP+ +V +PLFCCKPSKNQL
Sbjct 61 ITYSIKQGDNFFILSITSYQNLNTYLEFKNFENPNLSPTLLPLDTKVSVPFLFCCKPSKNQL 120
Query 173 DRGIKYLITHVWQPNNDVSVFVSNKLGASPDILSENNYGQNF TAASNLPVLIPVTLPLDL 232
++GKIYLIT+VWQ NDNV+ VS+K GAS ++L+ENN+ NFTA++N VLIPVT LP L
Sbjct 121 NKGIKYLITYVWQNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLI PVTSLPKL 178
Query 233 IQSPSDGRKHRI-GLPVIIGISLGCTLLVVVSAILLVVCVCLKMKSLNRSASSAETADKL 291
Q S+GRK L +IIGISLG ++V + LV V CLKMK LNRS SS+ETADKL
Sbjct 179 DQPSNNGRKSQNLALIIIGISLGAFFILVLTLSLVYVYCLMKRLNRSSTSETADKL 238
Query 292 LSGVS 296
LSGVS
Sbjct 239 LSGVS 243

```

>dbj|BAI79278.1| LysM type receptor kinase [Lotus japonicus]
Length=666



Score = 293 bits (750), Expect = 5e-77, Method: Compositional matrix adjust.
Identities = 192/636 (30%), Positives = 328/636 (51%), Gaps = 99/636 (15%)

```

Query 14 ILYVVLMEFTCI----EAQSQQTNGTNFSCFPS-----NSPPSCETYVTVYISQSPN 59
+L V+++ F+ + +AQ+ N C + NS SC++Y+T+ S SP
Sbjct 18 LLLVMIISFSHMIPSTQAQQEYVNNKQLDCDTQYNTTYGNVCNSVTSCQSYLTFKSSSPE 77
Query 60 FLSLTSSVNI FDTSPLSIARASNLOHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQ 119
+ + +S+S + +++P +A+++N+ + +I ++ +PVTC C+G R N +Y + +
Sbjct 78 YNTPSSNISYLLNSTPSLIVAKSNIT-DVTPIITDVTVPVTCSCSGGRYQHNATYNLKK 136
Query 120 -GDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIVVPLFCCKPSKNQLDRGIKY 178
G++++ +A YQ+LT A+M NP ++ L G + +PL C CP+K Q D G KY
Sbjct 137 TGETYFSIANNTYQSLTTCQALMAQNPYDAK-NLFAGDDLHVPLRCACPTKKQSDAGFKY 195
Query 179 LITHVWQPNNDVSVFVSNKLGASPDILSENNYGQNF TAASNLPVLIPV-TLLPDLIQ--- 234
L+T++ ++ ++ G Q +L N P+L+P+ T P +Q
Sbjct 196 LLTYLVSQGESPDIAEIFGVDTQSVLDANELDSKSVFYFTPLLVLKTEPPARLQIAA 255
Query 235 -----SPSDGRKHRIGLPIIIGISLGCTLLVVVSAILLVVCVCL----- 273
S S +K VI+G+++G + +VV+ LLV C
Sbjct 256 SPPEPPPPAPAGNDS SSSSKW-----VIVGVTVGVAVCLVVA--LLVFLCFYNRRRRQ 308
Query 274 -----MKSLNRSASSAETADKLLSGVSGYVSKPTMYETGAILEATMNLSE 319
+K ++ + +E+ GV + T Y+ G I AT SE
Sbjct 309 PAPPVSVKDFPDPSAVKMSSETPTTESWSLSSEGVRAYATESLTAYKFGDIQTATKFFSE 368
Query 320 QCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHNGLVKLMGVSSDNDGNCFVVY 379
+ KI SVY+A+ +G AVK DV+ E+ +L+++NH N++L G + GN ++VY
Sbjct 369 ENKIKGSVYRASFKGDAAVKILNGDVSAEINLLKRINHANIIRLSGFCV-HKGN TYLVY 427
Query 380 EYAENGSLLEEWLFAKSCSETSNSRTSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDIT 439
E+AEN SL++WL + + S SL+W QR+ IA DV+ L Y+H + P +H+++
Sbjct 428 EFAENDSLDOWLHSDKKYQNS---VLSWMQVRQIAYDVADALNYLHNYTNPPIHIKNLK 484
Query 440 SSNILLDSNFKAKIANFSMARTFTNP-----MMSKID 471
S N+LLD F+AK++NF +AR + + K+D
Sbjct 485 SGNVLLDGKFRAKVSNFGLARVMEDQGEDGGFQMRHVVGTVQGYMPPEYIESGLITPKMD 544
Query 472 VFAFGVVLIELLTGRKAMTTKEN---GEVVMWKDIWKIFDQENREERLRKWMDPKLDN 528
VFAPGVV++ELL+GR+A ++ E GE ML + + + + +N ++LR +MDP L +

```



Sbjct 545 VFAGVVMLELLSGREATSSGEKNGLGENKMLSETVNHVL-EGDNVRDKLRGFMPTLRD 603
 Query 529 YYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSLS 564
 YP+D A S+A +A C A SRP I+E++++LS
 Sbjct 604 EYPLDLAYSMAEIAKRCVAHDLNSRPNISEVLMTSL 639


>ref|XP_001783589.1|  predicted protein [Physcomitrella patens subsp. patens]
 gb|EDQ51621.1|  predicted protein [Physcomitrella patens subsp. patens]
 Length=637

GENE ID: 5946784 PHYPADRAFT_152558 | hypothetical protein
 [Physcomitrella patens subsp. patens] (10 or fewer PubMed links)

Score = 285 bits (729), Expect = 1e-74, Method: Compositional matrix adjust.
 Identities = 193/614 (31%), Positives = 310/614 (50%), Gaps = 77/614 (12%)

Query 27 AQSQQTNGTNFSCPSNSPPS---CETYVTYISQSPNFLSLTSVSNIFDTSPLSIARAS-- 81
 AQ + ++C N+ PS C T+ Y + SL V + F+ + ++A S
 Sbjct 2 AQQNYNDETEGYAC--NAAPSSTSCSTFAFYRTFQAG-ESLRKVG DYFNKTA AAVANVSGM 58
 Query 82 NLQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGD SFYFVATTL YQNLTNWHAVM 141
 NL L Q L +P+ C C C RS +S+ I +GD+F+ ++ T Y LT + A+M
 Sbjct 59 NLLSTTASLKTQALYVPLDCRCLNARSQM QVSH TIVKGD TFWLLSVTEYGG LTRYQAMM 118
 Query 142 DLNPGLSQFTLPIG IQVVIPLFCCKPSKNQLDRGIKYLITHVWQPNDNVSVFNKLGASP 201
 NP + L IG + +P+FC CP+ Q+ G YL+T P++ + +S+ G S
 Sbjct 119 ASNPSKDVYNLTIGDTITVPIFCACPTAAQVANGTNYLVTTTVPSETLDII SARFGIST 178
 Query 202 QDILSENNYGQNF TAASNLPVLIPVTLPLD-----IQSPSDG--- 239
 D+ NN + N +L+P+ LP L + SP+
 Sbjct 179 TDLSRANNVNSSSILDVNTTLLVPLATLPPLATMDWAPVTSQPPPPSPATVASENAAPAV 238
 Query 240 -RKHRIGLPVIGISLGCTLLVVVSAILLVCCCLMKSLNRSASSAETADK-----L 291
 K P+ IGI++G L + + L+ + S + E + L
 Sbjct 239 ITKSASQTPLYIGIAGVAGFLTLAAV FALLLLFKASRNSGKPKDLTEEMKRPNMVHLEL 298
 Query 292 LSGVSGYVS--KPTMYETGAILEATMNLSECKIGESVYKANIEGKVLAVKRFKEDVTEE 349
 L+G+S V KP + I AT S + I SVYK I G+++A+K K ++T+E
 Sbjct 299 LAGMSDMVSGSEKPVLLSHEEQSATQGFSPENFIQGSVYKGCINGQLVAIKQMKGNMTQE 358
 Query 350 LKILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSL EEWLFAKSC---SETSNSRTSL 406
 LKIL +V+H NLVKL+G+ N ++VVEYA++GSL + L ++ + S S L
 Sbjct 359 LKILCQVHNSNLVKLVGLCVGGSENLYLVVEYAKHGLSLNDCLRNQA AIGRTTFSQSAAYL 418
 Query 407 TWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTN-- 464
 WC R+ IA+DV+ GL+Y+H + P VH+D+ +SNILLD NF+AK+ANF MA++ +
 Sbjct 419 FWC SRVRIALDVASGLE YIHNYTNPSFVHKDVKT SNILLDENFRAKVANFGMAKSAASAD 478
 Query 465 --PMMS-----KIDVFAFGVVLI ELLTGRKAMTTKENG EVVML 500
 P+++ K DV+AFGVV++E+L+G++A+ E E
 Sbjct 479 AGPLLTRHITGTQGYMAPEYLEHGLTVKADVYAFGVVLEILSGKEAVVRPEKDEEEQG 538
 Query 501 WKD-----IWKIFDQ--EENREERLRKWM DPKLDNYYPIDYALSLASLAVNCTADKSL 552
 K+ I + + E + E+LRK++DP+L + YPI+ A S+ASLA+ C
 Sbjct 539 VKERALSDIIVDVNLNAGTAE LQTEQLRK FIDPQLHSAYPIEIASIASLAMTCIDPDP AV 598
 Query 553 RPTIAEIVLSLSLL 566
 RP++ ++ +LS +
 Sbjct 599 RPSMKDVT FALSKM 612

>ref|XP_002326901.1|  predicted protein [Populus trichocarpa]

gb|EEE73651.1|  predicted protein [Populus trichocarpa]
 Length=609

GENE ID: 7470467 POPTRDRAFT_591844 | hypothetical protein [Populus trichocarpa]
 (10 or fewer PubMed links)


Score = 285 bits (728), Expect = 1e-74, Method: Compositional matrix adjust.
 Identities = 185/556 (33%), Positives = 295/556 (53%), Gaps = 54/556 (9%)


Query 46 SCETYVTYISQSPNFLSLTSVSNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCT 105
 SC+ ++ + SQ P+E S+ S+S + + +AR+N+ + +V+ +PV C C
 Sbjct 54 SCQAFLIFKSQ-PSFNSVPSISALTSANQEELARINNVTRLSEFPTNNEVI-VPVNCFCF 111
 Query 106 GNRSFANISYEINQG-DSFYFVATTL YQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFC 164
 G AN + ++ R ++Y +A Y+ L+ A+ LN ++ L G ++ +PL C
 Sbjct 112 GQYYQANTTIQVTTTRGTYYVIANETYEGLSTCAALKHLNIH-GEYDLLPGEELQVPLRC 170
 Query 165 KCPSKNQLDRGIKYLITHVWQPNDNVSVFNKLGASQDILSENNYGQNF TAASNLPVLI 224
 CP+ NQ+ RG KYL+T+ +DN+ ++++ S +DIL N +N T + +LI
 Sbjct 171 ACPTTNQMIRGTYLVTYPLSSDDNIPDIADRFKVS TKDILDANGMEENPTLYPD TTILI 230
 Query 225 PVTLLPDLIQS-----PS-----DGRKHRIGLPVIGISLGCTLLVVVSAILLVCV 270
 P+ P Q+ PS R + G++ C+LLV+ +V +
 Sbjct 231 PLPTQPTSSQTIIHSNPNISPPSALS PRNRGSKKKHYESAGLAAACSLVISIITAVVFL 290
 Query 271 CCLKMK----SLNRSASSAETADKLLSGVSGYVSKPTMYETGAILEATMNLSECKIGES 326
 C K + A D + ++ Y +++ + +AT NLS + +I S
 Sbjct 291 SCKKTREKVSGRGRERKQAVPED-IRVEIASYEQVLKVFKFEEVRKATENLSSES RINGS 349
 Query 327 VYKANIEGKVLAVKRFKEDVTEELKILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENG 386
 VY+ G++LAVK+ DVT+E+ IL+++NH NL+KL GV +N G ++V EY ENGS
 Sbjct 350 VYRGEFGGEILAVKKMSRDVTKEVNILKRINHFNLIKLEGVC-ENRGCFYLVLEYMENG 408
 Query 387 LEEWLFAKSCSETSNRTSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLD 446
 L EWL K ET N W QRI IA+DV+ GL Y+H P VH+DI SSN+LL+
 Sbjct 409 LREWLSCKKFEETGN-----WAQRIQIALDVANGLYLHSFTEPAYVHKDIKSSVLLN 462
 Query 447 SNFKAKIANFSMARTFTNPMMS-----KIDVFAFGVVLI ELLT 484
 N +AKIANFS+AR T+ M+ KIDV+AFGV+L+EL+T
 Sbjct 463 GNLRKAKIANFSLARAATSAAMTKHVVGSI GYMAPEYVREGQVTPKIDVYAFGVILLELIT 522
 Query 485 GRKAMTTKENG EVVMLWKDIWKIFDQ EENREERLRKWM DPKLDNYYPIDYALSLASLAVN 544

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Sbjct 523      G+ A+ T ++G  +L  +I+ I +  +N E L  ++DP L      ++AL LA ++V
      GKDAVFT-QDGREALLSTEIFSIMEN-KNPEVELDFVDPALKGSCGTNFALCLAKVSVA 580
Query 545      CTADKSLSRPTIAEIV 560
      C  +  RP++ E+V
Sbjct 581      CLMKEPARRPSMEEVV 596

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>ref|XP_002510756.1|  kinase, putative [Ricinus communis]

gb|EEF52943.1|  kinase, putative [Ricinus communis]
Length=634

GENE ID: 8269969 RCOM_1602540 | kinase, putative [Ricinus communis]

Score = 284 bits (727), Expect = 2e-74, Method: Compositional matrix adjust.
Identities = 188/575 (32%), Positives = 291/575 (50%), Gaps = 80/575 (13%)

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Query 46      SCETVYVYISQSPNFLSLTSVSNIF---DTSPLSIARASNLQHEEDKLIPGQVLLIPVTC 102
      SC++Y+T+ S P + + ++S +F D++ L IA +N+ + + P L IPV C
Sbjct 56      SCQSYLTFRSAPPYYTTPVTISYLFSLQDSASL-IASLNNISSDVSSIIPPQSOLFIPVNC 114

Query 103     GCTGNRSFA-NISYEINQGDSFYF-VATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVI 160
      C G + + N SY + YF VA YQ L+ A+M NP L +G+++ +
Sbjct 115     SCFGGQFYQHNASYTTLKFSSETYFSVANDTYQGLSTCQALMSQNP-YGDRNLSVGMRLQV 173

Query 161     PLFCKCPSKNQLDRGIKYLITHVWQPNNDNVSFVSNKLGASPDILSENNGQNFTAASNL 220
      PL C CP+ NQ G +YL+T++ D +S ++ G PQ IL N
Sbjct 174     PLRCACPTSNQALGFFRYLLTYMVTWGDITISSIAELFGVRFQSILDANQLSSTSIIFFPT 233

Query 221     FVLIPVTLPLDLIQS-----PSDGRKHRIGLPVIIIGISLGCTLLVV--V 262
      P+L+P+T P I++ PS G + +G+ LG LL++ V
Sbjct 234     PILLVPLTTPPTTIKASPPPPVVSPPPLTPVLPSGSSSRKW---TYVGVGLGAALLLIFAV 290

Query 263     SAILL-----VCVCCLKMKSL--NRSASSAETADKLLSGVSGYVSKPTMYETGAIL 311
      S L + + K+L + SA +++ G + T+Y+ +
Sbjct 291     SGFLFWYPKSKSRKLTTPVPIPSKALQSDSSAVPPDSSTPWSRSAYGVIESLTLTKFHDQL 350

Query 312     EATMNLSEQQKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNNLVKLMGVSSDN 371
      AT SE+ +I SVYK + +G AVK K DV+ E+ IL+K+NH N+++L GV
Sbjct 351     LATDYFSEKNRIKGSVYKGSFKGDAAAVKVMKGDVSEISILKKINHSNIIRLSGVCL-Y 409

Query 372     DGNCFVYVEYAENGSLLEWLFAKSCSETSNRSRTSLTWCQRISIAVDVSMGLQYMHEHAYP 431
      D N ++VYE+AENGSL E N +T LTW QR+ IA DV+ L Y+H + P
Sbjct 410     DANTYLVYFEAENGSLAE-----NVQT-LTWKQVRVQIAHDVADALNLYLHNYTNP 457

Query 432     RIVHRDITSSNILLDSNFKAKIANFSMARTFTNP----- 465
      +H+++ +SNILLD+N +AKIANF +ART N
Sbjct 458     PYIHKNLKTSNILLDANMRKIANFGLARTLQNEAEGGLHLTRHVVGTVQGYMAPEYMENG 517

Query 466     -MMSKIDVFAFGVVLIELLTGRKAMTTKENGVEVMLWKDIWKIFDQENREERLRKWMMDP 524
      + K+DVFAFGVV++ELL+G++A T +N ML I ++ + +N +L +MDP
Sbjct 518     VITPKLDVFAFGVVLIELLSGKEAATYDKNAREEMLSASICRVL-EGDNVRHKLKCGFMDP 576

Query 525     KLDNYYPIDYALSLASLAVNCTADKSLSRPTIAEI 559
      L YP+D A SLA LA C + +RP+++++
Sbjct 577     SLGKQYPLDLAFLSLAQLAQTCTISHDINARPSVSQV 611

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>dbj|BAI79277.1| LysM type receptor kinase [Lotus japonicus]

dbj|BAI79287.1| LysM type receptor kinase [Lotus japonicus]
Length=667

Score = 283 bits (724), Expect = 5e-74, Method: Compositional matrix adjust.
Identities = 193/663 (29%), Positives = 339/663 (51%), Gaps = 104/663 (15%)

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Query 18      VLMFECTCIEAQSQQ-----TNGTNFSCPSNSPPSCETVYVYISQSPNFLSLTS 65
      + F E Q+QQ T+ + + NS SC++Y+T+ S SP + + +S
Sbjct 21      AMSFHMISEEQAQEQEYLNNNQLDCDNTHNSTYGNVCNSVTSCQSYLTFKSSSPEYNTPSS 80

Query 66      VSNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQ-GDSFY 124
      +S + +++P +A+++N+ + +I ++ +PVTC C+G R N +Y + + G++++
Sbjct 81      ISYLLNTPSLVAKSNIT-DVTPIIITDTMTVTVPTVTCSSGGRYQHNAATYNLKKTGETYF 139

Query 125     FVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHVW 184
      +A YQ+LT A+M NP ++ L G + +PL C CP+K Q D G KYL+T++
Sbjct 140     SIANNNTYQSLTTCQALMAQNPYDAK-NLFAGDDLHVPLRCACPTKKQSDAGFKYLLTYLV 198

Query 185     QPNDNVSFVSNKLGASPDILSENNGQNFTAASNLVLIPIV-TLLPDLIQ----- 234
      ++ ++ G Q+L N P+L+P+ T P +Q
Sbjct 199     SQGESPDISAEIFGVDTQSVLDANELDSKSVVYFTPLLVPLKTEPPARLQIAASPPESP 258

Query 235     -----SPSDGRKHRIGLPVIIIGISLGCTLLVVVSAILLVVCVCL----- 273
      S S +K VI+G+++G + +VV+ LLV C
Sbjct 259     PPAPAGNDSSSSSKKW-----VIVGVTVGVAVCLVVA--LLVFLCFYNRRRRQPAPPPV 311

Query 274     -----KMKSLNRSASSAETADKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGE 325
      +K ++ + + E+ GV + T Y+ G I AT SE+ KI
Sbjct 312     SVKDFPDSAVKVMVSETPTTESWSLSSEGVRYAIESLTAYKFGDIQTATKFFSEENKIKG 371

Query 326     SVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNNLVKLMGVSSDN DGNCFVYVEYAENG 385
      SVY+A+ +G AVK DV+ E+ +L+++NH N+++L G + GN ++VYE+AEN
Sbjct 372     SVYRASFKGDDAAVKILNGDVSAEINLLKRINHANIIRLSGFCV-HKGNTYLVYFEAEND 430

Query 386     SLEEWLFAKSCSETSNRSRTSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILL 445
      SL++WL ++ + S SL+W QR+ IA DV+ L Y+H + P ++H+++ S N+LL
Sbjct 431     SLDDWLHSEKKYQNS---VLSLWMQVRVQIAYDVADALNLYLHNYTNPVLIHKNLKS GNVL 487

Query 446     DSNFKAKIANFSMARTFTNP-----MMSKIDVFAFG 476
      + F+AK++NF +AR + + K+DV+AFG
Sbjct 488     NGKFRKVSFNFLARAMEQGEDGGGFQMTRHVVGTVQGYMPPEYTENGLITPKMDVYAFG 547

Query 477     VVLELLTGRKAMTTKEN---GEVVMWLWKDIWKIFDQE-ENREERLRKWMDPKLDNYPI 532
      VV++ELL+L+ + GE ++L+ + + + +N ++LR +MD L + YP+
Sbjct 548     VVMLELLSGKEATGNGDKNGLGKVMVLETVNHHVLEGNDNDNRDKLRGFMQTLRDEYPL 607

Query 533     DYALSLASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATLERSLTSSGLDVEATQIVT 592
      D A S+A +A C A SRP I+E+ ++LS + +TL+ +S +VE ++ V+

```

Sbjct 608 DLAYSMAEIAKRCVAHDLNSRPNISEVFM TLS---KVQSSTLDWDPSS---EVERSRSVS 661
 Query 593 SIS 595
 IS
 Sbjct 662 QIS 664

>emb|CB117583.3| unnamed protein product [Vitis vinifera]
 Length=1305

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position
 Score = 277 bits (708), Expect = 3e-72, Method: Compositional matrix adjust.
 Identities = 182/594 (30%), Positives = 305/594 (51%), Gaps = 70/594 (11%)

Query 16 YVLMFFTCIEAQSQQTNGTNFSCPSNSPPSCETYVYIISQSPNFLSLTSVSNIFDTSPL 75
 Y ++ +TC NG N +C+TY+ + S+SP + ++S+S++ + P
 Sbjct 705 YTTVLGYTC-----NGVN-----TTCQTYLIFRSESP-YNNVSSISDLLASDPS 747
 Query 76 SIARASNQLQHEEDKLIPGVLLIPVTCGCTGNRSFANISYEINQGDSEFYFVATTLYQNLT 135
 +A+ +++ E + +++PV C C+GN S N SY + GD ++A +Q L+
 Sbjct 748 QLAQINSVT-ETATFDTNKEVIVPVNCSGNYSTNTSYVVKNGDYPLWIANNFTQGLS 806
 Query 136 NWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHVWQPNNDVSEFVN 195
 A+++ NP +S L G + +PL C CP+K Q D G+KYL++++ D VS +S
 Sbjct 807 TCQALLNQNPFSVSATNLNPGTSITVPLRCACPTKQSDAGVKYLSYLVAYGDTVSAISG 866
 Query 196 KLGASPDILSENNYQNFATAASNLPLVLPVTLPLDILQSPSDGRKHRIGLPVLIIGISLG 255
 + G + L N + T +LIP L PS + + + VI+G++ G
 Sbjct 867 RRGVDTERTLEANESEQDTINPFTLLIP-----LQNPPSSSQTIKTWVYVIVGVAAG 920
 Query 256 CTLLVVVSAILLVVCVCLMKMSLNRSASSAET-----ADKLLSGVSGYVSKPTM 304
 LL+ ++ V K K N + +E+ + +S +
 Sbjct 921 VLLLLFFGVIVFKF-FRKTKKNDQIAVSESFKPLEKPLKVEEHEFFESISMAQSVKV 979
 Query 305 YETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHNHNLVKL 364
 Y+ + AT N S C I SVY+ I+G + A+K+ +V+ E+ +L K+NH N+++L
 Sbjct 980 YKFEELQSATDNFSPSCLIKGSVYRGTIKGDAAIKKMDGNVSNEIALLSKINHFNIVRL 1039
 Query 365 MGVSSDNDGNCVFVVEYAENGSLLEWLFKSCSETSNRSRTSLTWCQRISIAVDVSMGLQY 424
 G+ NDG+ ++V+EYA NGSL +W++ +N R L W QRI IA+DV+ GL Y
 Sbjct 1040 SGICF-NDGHWYLVHEYAVNGSLSDWIYYN-----NNDRRFLVWTQRIQIALDVATGLNY 1093
 Query 425 MHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMART----- 461
 +H H P +H+D+ S+N+LLD +F+AKIANF AR+
 Sbjct 1094 LHIHVSFYSYIHKDKMSNNVLLDGDFAKIANFDQARSAGQEGQFALTRHIVGTKGYMAP 1153
 Query 462 --FTNPMMS-KIDVFAFGVVLIELLTGRKAMTTKENGVEVWLWKDIWKIFDQENREERL 518
 N ++S K+DV+AFGV+++E+ TC K + GE + L + + E++ +E+L
 Sbjct 1154 EYLENGLISTKLDVYAFGVLMLEIFTG-KEVAALYGESIHLEVLAAVL-HEDDGKEKL 1211
 Query 519 RKWMDPKLDNYYPIDYALSASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPA 572
 ++DP LD YP + A+ + L +C RP + EIV SLS + S A
 Sbjct 1212 GDFIDPSLDGNYPELAIFMIRLIDSCLTAKAPAGRPDMDEIVQSLSRILASSQA 1265

Score = 265 bits (676), Expect = 2e-68, Method: Compositional matrix adjust.
 Identities = 173/557 (31%), Positives = 293/557 (52%), Gaps = 56/557 (10%)

Query 46 SCETYVYIISQSPNFLSLTSVSNIFDTSPLSIARASNQLQHEEDKLIPGVLLIPVTCGCT 105
 SC+ ++ + S+ P + ++S+S++ + P +A+ +++ E + +++PV C C+
 Sbjct 74 SCQAFLIFRSEPP-YNDVSSISDLLGSDPSQLAQINSVD-ETATFETKKEVIVPVNCSGS 131
 Query 106 GNRSFANISYEINQGDSEFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCK 165
 G S AN SY + GD++ +A ++ L+ A+ L+ + G ++ +PL C
 Sbjct 132 GEFSQANTSYVVQHGDTYLLIANNTFEGLSTCQALRSQRTSLTT-NIYTGKLTVPRLCA 190
 Query 166 CPSKNQLDRGIKYLITHVWQPNNDVSEFVNKLGASPDILSENNYG-QNFTAASNLPLVI 224
 CP+KNQ D G+KYL++++ D VS +S + G L N QN P +
 Sbjct 191 CPTKNQSDVGVKYLMSYLVASGDYVSSISVRFGVDTGMTLEANESEQN-----PNII 243
 Query 225 P-VTLLPDILQSPSDGRKHRIGLPVLIIGISLGTLLVVVSAILLVVCVCLMKMSLNRSAS 283
 P TLL L PS + + + V+G+ G L+++ ++ K + A
 Sbjct 244 PFTLLIPLQLNPPSSSQTIKTWVYVVGVSAGSALVLLFGSVIFFKFRKTRKKTDPIDAI 303
 Query 284 S-----AETADKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIE 333
 S E + L +S +Y+ + AT N S C+I SVY+ I+
 Sbjct 304 SESFEACEKPLKEEQHEFLESISSIAQSLKVYFEELQSATDNFSPNCRKIGSVYRGTIK 363
 Query 334 GKVLAVKRFKEDVTEELKILQKVNHNHNLVKLMGVSSDNDGNCVFVVEYAENGSLLEWLF 393
 G + A+K+ +V+ E+ +L K+NH N+++L G+ NDG+ ++V+EYA NG L +W++
 Sbjct 364 GDAAIKKMDGEVSNEIALLNKINHFNIVRLSGICF-NDGHWYLVHEYAVNGPLTDWIY- 421
 Query 394 KSCSETSNRSRTSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKI 453
 + +SR L W QRI IA+DV+ GL Y+H + P VH+DI S N+LLDS+F+AKI
 Sbjct 422 ---NNDDSRF-LVWMQRIQIALDVATGLNLYHSYTSPPYVHKDIKSGNVLLDSDFRAKI 477
 Query 454 ANFSMART-----FTNPMMS-KIDVFAFGVVLIELLTGRK 487
 ANF +AR+ N ++S K+DV+AFGV+++E+LTG++
 Sbjct 478 ANGLARSAGQEGQFALTRHIIGTRGYMAPEYLENGLVSTKLDVYAFGVLMLEMLTGKE 537
 Query 488 AMTTKENGVEVWLWKDIWKIFDQENREERLRKWMDPKLDNYYPIDYALSASLAVNCTA 547
 E GE + L D+ E + +E+LR ++DP L YP++ A+ + L +C
 Sbjct 538 VAALYE-GENMHL-PDVLVAVLHEGDGKEKLRNFIDPSLSGNYPELAIVMIRLIDSLCK 595
 Query 548 DKSLSRPTIAEIVLSLS 564
 SRP + EIV +LS
 Sbjct 596 KSPASRPDMVEIVQALS 612

>ref|XP_002990805.1| [S] hypothetical protein SELMODRAFT_11326 [Selaginella moellendorffii]
 gb|EFJ08078.1| [S] hypothetical protein SELMODRAFT_11326 [Selaginella moellendorffii]
 Length=539

GENE ID: 9659107 SELMODRAFT_11326 | hypothetical protein

[Selaginella moellendorffii]

Score = 275 bits (702), Expect = 2e-71, Method: Compositional matrix adjust.
Identities = 187/552 (33%), Positives = 287/552 (51%), Gaps = 31/552 (5%)

```
Query 37 FSCPSNSPPSCETVTVYISQSPNFLSLTSVSNIFDTSPLSIARASNLQHEEDKLI PGQVL 96
+SC SNS SC+ Y Y + + +L SV F S +A AS + + L+P QVL
Sbjct 1 YSCVSNST-SCQAYAAAYRALQGD--TLQSVGLRFRLSVEQLAEASQIA-QSATLVDPQVL 56

Query 97 LIPVTCGCTGNRSFANISYEINQGDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGI 156
LIP+ C C RS N +Y I GD+ Y V+ +Q LT + AV NP L G
Sbjct 57 LIPLNCSCASGRSQFNATYIIQSGDTLYLVSNGTFFQGLTTYQAVERANPLAVPTNLQPGD 116

Query 157 QVVIPLEFCKCPSKNQDRGIKYLITHVWQPNNDVSVFVSNKLGASPDILSENNYGQNFTA 216
+V P+ C CPS Q+ G+ L+T+ P + + ++ S + S+N + T
Sbjct 117 SIVFPIRCACFPSSAQVAAGVTSLVYTSIWPGEILDGIARAWNVSRTLASDNTVSGSATL 176

Query 217 ASNLPLVLIPTLLPDLIQSPSDGRKHRIGLPVFIIGISLGTLLVVVSAILLVCVCCCLKMK 276
+ P S G+ +GI++ C V++ + LV + +
Sbjct 177 SPAAPPPANNPPNNSPSPDSSSSSGSNTGM--YVGIACVACVAALLVVVALVIFYRRRSR 234

Query 277 SLNRSASSAETADK-----LLSGVSGYVS--KPTMYETGAILEATMNLSEQCKIGESV 327
+ +++S AE + + LL+G+ G V +P ++ + +AT N S I SV
Sbjct 235 KVTKASSYAEPSKEQSPHAPLLAGMHGLVDSERPVVFSEYELCDATNNFSASHLIQGSV 294



Query 328 YKANIEGKVLAVKRFKEDVT-EELKILQKVHGNLVKLMGVSSDNDGNCFFVVEYAENG 386
Y+ + +++A+K K T +ELKIL KV+H NLVKL+G+ S +D F+VVEYA+NGS
Sbjct 295 YRGILRKQLVAIKEMKGGTTSQELKILCKVHHSNLVKLIGICSGDD-KLFLVVEYADNGS 353

Query 387 LEEWLFKSCSETSNRSTSLTWQCRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLD 446
L SC + W R+ +A+DV+ GL+Y+H++ P VH+D+ SSNILLD
Sbjct 354 LS-----SCLHNRTPAATAIWNTRLQVAMDVATGLEYIHDYTKPSFVHKDVKSSNILLD 407

Query 447 SNFKAKIANFSMARTFTNP--MMSKIDVFAFGVVLIELLTGRKAMTTKENGVEVMLWKDI 504
+N +AK+ANF MAR + + +K+DV+AFGVVL+EL TGR+A+ + G D
Sbjct 408 ANLRKAVANFGMARLYLTHGFVTTKVDVYAFGVVLELFTGREAILSTGTGSEKQYLADA 467

Query 505 W----KIFDQENRE--ERLRKWMDPKLDNYYPIDYALSASLAVNCTADKSLSRPTIAE 558
+ F ++N E E+L+ W DP LDN P D AL+ +A +C +RP + +
Sbjct 468 FVKLTGDFAGDDNDEKIEKLKHWDPILDNAVFPWDIALNFVEVARSCVDADPDARPNMKD 527

Query 559 IVLSLSLLTQPS 570
+ LS L + S
Sbjct 528 VTFKLSKLESS 539
```

>ref|XP_002974494.1|  hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii]
gb|EFJ24716.1|  hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii]
Length=539

GENE ID: 9657733 SELMODRAFT_11327 | hypothetical protein
[Selaginella moellendorffii]

Score = 273 bits (699), Expect = 4e-71, Method: Compositional matrix adjust.
Identities = 187/552 (33%), Positives = 286/552 (51%), Gaps = 31/552 (5%)

```
Query 37 FSCPSNSPPSCETVTVYISQSPNFLSLTSVSNIFDTSPLSIARASNLQHEEDKLI PGQVL 96
+SC SNS SC+ Y Y + + +L SV F S +A AS + + L+P QVL
Sbjct 1 YSCVSNST-SCQAYAAAYRALQGD--TLQSVGLRFRLSVEQLAEASQIA-QSATLVDPQVL 56

Query 97 LIPVTCGCTGNRSFANISYEINQGDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGI 156
LIP+ C C RS N +Y I GD+ Y V+ +Q LT + AV NP L G
Sbjct 57 LIPLNCSCASGRSQFNATYIIQSGDTLYLVSNGTFFQGLTTYQAVERANPLAVPTNLQPGD 116

Query 157 QVVIPLEFCKCPSKNQDRGIKYLITHVWQPNNDVSVFVSNKLGASPDILSENNYGQNFTA 216
+V P+ C CPS Q+ G+ L+T+ P + + ++ S + S+N + T
Sbjct 117 SIVFPIRCACFPSSAQVAAGVTSLVYTSIWPGEILDGIARAWNVSRTLASDNTVSGSATL 176

Query 217 ASNLPLVLIPTLLPDLIQSPSDGRKHRIGLPVFIIGISLGTLLVVVSAILLVCVCCCLKMK 276
+ P S G+ +GI++ C V++ + LV + +
Sbjct 177 SPAAPPPANNPPNNSPSPDSSSSSGSNTGM--YVGIACVACVAALLVVVALVIFYRRRPR 234

Query 277 SLNRSASSAETADK-----LLSGVSGYVS--KPTMYETGAILEATMNLSEQCKIGESV 327
+ +++S AE + + LL+G+ G V +P ++ + +AT N S I SV
Sbjct 235 KVTKASSYAEPSKEQSPHAPLLAGMHGLVDSERPVVFSEYELCDATNNFSASHLIQGSV 294


Query 328 YKANIEGKVLAVKRFKEDVT-EELKILQKVHGNLVKLMGVSSDNDGNCFFVVEYAENG 386
Y+ + +++A+K K T +ELKIL KV+H NLVKL+G+ S +D F+VVEYA+NGS
Sbjct 295 YRGILRKQLVAIKEMKGGTTSQELKILCKVHHSNLVKLIGICSGDD-KLFLVVEYADNGS 353

Query 387 LEEWLFKSCSETSNRSTSLTWQCRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLD 446
L SC + W R+ +A+DV+ GL+Y+H++ P VH+D+ SSNILLD
Sbjct 354 LS-----SCLHNRTPAATAIWNTRLQVAMDVATGLEYIHDYTKPSFVHKDVKSSNILLD 407

Query 447 SNFKAKIANFSMARTFTNP--MMSKIDVFAFGVVLIELLTGRKAMTTKENGVEVMLWKDI 504
+N +AK+ANF MAR + + +K+DV+AFGVVL+EL TGR+A+ + G D
Sbjct 408 ANLRKAVANFGMARLYLTHGFVTTKVDVYAFGVVLELFTGREAILSTGTGSEKQYLADA 467

Query 505 W----KIFDQENRE--ERLRKWMDPKLDNYYPIDYALSASLAVNCTADKSLSRPTIAE 558
+ F ++N E E+L+ W DP LDN P D AL+ +A +C +RP + +
Sbjct 468 FVKLTGDFAGDDNDEKIEKLKHWDPILDNAVFPWDIALNFVEVARSCVDADPDARPNMKD 527

Query 559 IVLSLSLLTQPS 570
+ LS L + S
Sbjct 528 VTFKLSKLESS 539
```

>ref|XP_002277331.1|  PREDICTED: hypothetical protein [Vitis vinifera]
Length=638

GENE ID: 100258108 LOC100258108 | hypothetical protein LOC100258108
[Vitis vinifera]

Score = 272 bits (696), Expect = 8e-71, Method: Compositional matrix adjust.
Identities = 183/599 (30%), Positives = 298/599 (49%), Gaps = 82/599 (13%)

```

Query 31 QTNGTNFSCPSNSPPSCETYVTYISQSPNFLSLTSVSNIFDTSPLSIARASNLOHEEDKL 90
+TNG F C N P SC +Y+T+ S P++ S S++ + ++ P IA + + + D +
Sbjct 32 ETNG--FQC--NGRPSCHSYLTFRSAPPSYDSPSIAYLNLNPEAQIATINEVS-DVDITI 86

Query 91 IPGQVLLIPVTCGCTGNRSFANISYEINQGDSFYF-VATTLYQNLTNWHAVMDLNPGLSQ 149
+VL++PV C C+G+ N +Y + YF +A YQ LT A+ NP
Sbjct 87 SKDTVLIVPVNCSGSGDFYQHNTTYTLKSASETYFSLANNTYQGLTTCQALKAQNP-YDY 145

Query 150 FTLPIGIQVVIPLFCCKPSKNQLDRGIKYLITHVWQPNNDNVSFVSNKLGASP-QDILSEN 208
+L +G+ + +PL C CP+ NQ G YL+++ D + ++ G Q I N
Sbjct 146 RNLSVGLHLQVPLMCACPTANQTAAGFNILLSYLVTWGDTIDSIAKIFGVDDVQSIYDAN 205

Query 209 NYGQNFTAASNLPVLIPVTLPLDIQS-----PSDGRKHRIGLPVIGIS 253
+P+L+E+ P IQ+ PS G + V IG
Sbjct 206 RLSSTSVIYPFTPLVPLKNPPSKIQTTVSSPPAPSPETPMVPSGGGSNSSKKWVFIGAG 265

Query 254 LGCTLLVV-VSAILLVCCCLMKMS-----LNRSSASSAETADKLLSGVSGY 298
+G LLV+ +S+ ++ C + +S L++S + + L G+
Sbjct 266 IGAALLVLLISSGMMFCFFRRRQSGQDKPVLDLGEATKLSKLENKTSMSISLEGIRIE 325

Query 299 VSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNH 358
+ T+Y+ + +A E +I SVY+A+ +G A+K K DV+EE+ IL+++NH
Sbjct 326 MESLTVKYEELQKAAGYFGEANRIKGSVYRASFKGDDAAIKMMKGDVSEEINILKQINH 385


Query 359 GNLVKLMGVSSDNDGNCVYVEYAENGSLLEWLFA--KSCSETSNRSTSLTWCQRISIAV 416
+++L G + GN ++VVEYAENG+L +WL ++CS ++L W QR+ IA
Sbjct 386 SKVIRLSGFCI-HAGNTYLVVEYAENGALRDWLHGDGETCS-----TLGWKQRVQIAY 437

Query 417 DVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNP----- 465
D + L Y+H P +H+++ SNILLD N + K+ NF +AR N
Sbjct 438 DAADALNYLHNFISSPPIHKNLKNISNILLDGNMRGKVTNFGLARRLGNEEGDGGGLQLTR 497

Query 466 -----MMSKIDVFAFGVVLIELLTGRKAMTT--KENGEEVVMWLDI 505
+ K+D+FAFGVV++ELLTG++A + KE GE++ + I
Sbjct 498 HVGVTQGYMAPEYVENGVTPLKLDIFAFGVVILELLTGKEAAPSQRKEGELLVSV--SIN 555

Query 506 KIFDQEEENREERLRKWMDPKLDNYYPIDYALSASLAVNCTADKSLSRPTIAEIVLSLS 564
++ Q+DN ++LR ++DP L + YP D A S+A LA +C A +RPT+++I + LS
Sbjct 556 EVL-QG NVNRDKLRGFDPCLAHEYFPDLAFSMAQLAKSCVAHDLNARPTMSDIFVILS 613

```

>ref|XP_002269442.1|  PREDICTED: hypothetical protein [Vitis vinifera]
Length=632

GENE ID: 100264999 LOC100264999 | hypothetical protein LOC100264999
[Vitis vinifera]

Score = 268 bits (685), Expect = 2e-69, Method: Compositional matrix adjust.
Identities = 182/611 (29%), Positives = 306/611 (50%), Gaps = 81/611 (13%)

```

Query 16 YVVMFFTCIEAQSQQTNGTNFSCPSNSPPSCETYVTYISQSPNFLSLTSVSNIFDTSPL 75
+Y ++ +TC NG N +C+TY+ + S+SP + ++S+S++ + P
Sbjct 40 YTTVLGYTC-----NGVN-----TTCQTYLIFRSESP-YNNVSSISDLLASDPS 82

Query 76 SIARASNLOHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSFYFVATTLYQNLT 135
+A+ +++ E + +++PV C C+GN S N SY + GD ++A +Q L+
Sbjct 83 QLAQINSVT-ETATFDTNKEVIVPVNCSGSGNYSQTNTSYVVKNGDYPLWIANNTFQGLS 141

Query 136 NWHAVMDLNPGLSQFTLPIGIQVVIPLFCCKPSKNQLDRGIKYLITHVWQPNNDNVSFVSN 195
+A+++ NP +S L G + +PL C CP+K Q D G+KYL+++ D VS +S
Sbjct 142 TCQALLQNPSPVSATNLNPGTSTVPLRCACPTKAQSDAGVKYLSYLVAYGDTVSAISG 201

Query 196 KLGASPDILSENNGYQNFATAASNLPVLIPVTLPLDIQS-----PSD 238
+ G + L N + T +LIP+ P Q+
Sbjct 202 RFGVDTERTEANELSEQDTINPFTTLLIPLQNPSSQTIVPPPPPPPPPSAVSSPS 261

Query 239 GRKHRIGLPVIGISLGCTLLVVVSAILLVCVCLMKMSLNRSSASSAET----- 287
G + + VI+G++ G LL+ ++ V K K N + +E+
Sbjct 262 GSSKKTVWYVIVGVAAGVLLLLFFGYVIFVKF-FRKTKKKNDQIAVSESFKPLEKPLKVE 320

Query 288 ADKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVT 347
+ +S +Y+ + AT N S C I SVY+ I+G + A+K+ +V+
Sbjct 321 EHEFFESISMAQSVKVKFEELQSATDNFSPCLIKGSVYRGTIKGDLLAAIKMDGNVS 380

Query 348 EELKILQKVNHNGLVKLMGVSSDNDGNCVYVEYAENGSLLEWLFAKSCSETSNRSTSLT 407
E+ +L K+NH N+++L G+ NDG+ ++V+EYA NCSL +W++ +N R L
Sbjct 381 NEIALLSKINHFNVRILSGICF-NDGHWYLVHEYAVNGSLSDWIYYN-----NNDRRFLV 434

Query 408 WCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMART----- 461
W QRI IA+DV+ GL Y+H H P +H+D+ S+N+LLD +F+AKIANF AR+
Sbjct 435 WTQRIQIALDVATGLNYLHIHVSPSYIHKDMKSNVLLDGDGFRKIANFDQARSAGQEG 494

Query 462 -----FTNPMS-KIDVFAFGVVLIELLTGRKAMTTKENGEEVVMW 501
N ++S K+DV+AFGV+++E+ TG K + GE + L
Sbjct 495 QFALTRHIVGTKGYMAPEYLENLISTKLDVYAFGVLMLEIFTG-KEVAALYGGESIHLS 553

Query 502 KDIWKIFDQEEENREERLRKWMDPKLDNYYPIDYALSASLAVNCTADKSLSRPTIAEIVL 561
+ + + E++ +E+L ++DP LD YP + A+ + L +C RP + EIV
Sbjct 554 EVLA AVL-HEDDGKEKLGDFIDPSLDGNYPPELAIFMIRLIDSLTKAPAGRPMDEIVQ 612

Query 562 SLSLLTQPSA 572
SLS + S A
Sbjct 613 SLSRILASSQA 623

```

>dbj|BAI79276.1| LysM type receptor kinase [Lotus japonicus]
Length=633

Score = 268 bits (684), Expect = 2e-69, Method: Compositional matrix adjust.
Identities = 204/659 (30%), Positives = 327/659 (49%), Gaps = 116/659 (17%)

```

Query 1 MAVFFVSLTLGAQILYVVMFFTC-IEAQSQQTNGTNFSCPSNSP-PSCEYVTYISQSP 58
+ +FF AQ Y+ L C S G ++C S +C+ Y+T+ +Q P
Sbjct 14 LFIFFTFPITLAQQPYIGLATNACPRRGNSNSIRG--YTCNGGSANHTCQAYLTFRTQ-P 70

Query 59 NFLSLTSVSNIFDTSPLSIAR----ASNLOHEEDKLIPGQVLLIPVTCGCTGNRSFANIS 114
+ S+ ++S + + +A + N E +KL+ ++PV C C G AN S

```

```

Sbjct 71 IYNSVYTISTLLSSDARHLAETMSVSNQNTTFETNKLV-----IVPVQCSCAGEYYQANTS 125
Query 115 YEINQGDsfYfVATTLYQNLTNWHAVM--DLNPGLSQFTLPIGIQVVIPLFCCKCPKSNQL 172
Y D+ + +A ++ LT A+M + NPG L +G ++ +PL C CP+KNQ
Sbjct 126 YAFQNTDTPFSIANNTFEGLTTCQALMHENHNPg----HLYLGRELTVPLRCACPTKNQT 181
Query 173 DRGKYLITHVWQPNNDNVSVSNKLGASPDILSENNYGNFTAAASNLPVLIPVTLTPDL 232
++GKYL+++ D+VS +S K G S + L N+ + T A P TLL L
Sbjct 182 EKGKYLSSLYVNWGDSVSVISEKFGVSCNNTLEANS--SLTKAKIYPF---TTLVPL 236
Query 233 IQSPSDGR-----KHRIGLPVIIGISLGCTLLVVVSAILLVC 269
PS+ + ++ L V++G G L+V++A++ C
Sbjct 237 HDKPSNSQTILQSQPSSTSSSPSSSTHQSSNKTWLYVVVG---GVFALIVLTAVIF-C 292
Query 270 VCCLMKSLNRSASSAETAD-----KLLSGVSGYVSKPTMYETGAILEA 313
+ K + + S S ++ KL + G +Y I A
Sbjct 293 IHYHKGRRKDDSLQLTVSESFENQQLGKEMKKGDGKLEFIHGIAQSFKVYSFEEIQRA 352
Query 314 TMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHNGLVLMGVSSDNDG 373
T NL+ I SVY+ + G ++A+K+ + DV++E++IL KVNH N+++L GVS N+G
Sbjct 353 TNNLNSSSLIKGSVYRGVMNGDLVAIKKTEGDVSKETQILKNVHNSNVIRLSGVSF-NEG 411
Query 374 NCFVVEYEAENGSLLEEWLFAKSCSETSNRSTSLTWCQRIISIAVDVSMGLQYMHEHAYPRI 433
++VVEYA NG L EW+F L+W QRI IA+DV++GL Y+H P
Sbjct 412 QWYLVEYEAANGPLSEWIFFGKF-----LSWTQRIQIALDVAIGLDYLHSFTSPPH 462
Query 434 VHRDITSSNILLDSNFKAKIANFSMART-----FTNPM 466
+H+D+ SSNILLDS+FAKIAN S+AR+ N +
Sbjct 463 IHKDLKSSNILLDSDFRAKIANLSLARSVKGVEDDDQFLATRNIVGTRGYMAPEYLENGL 522
Query 467 MS-KIDVFAFGVVLIELLTGRK--AMTTKENGVEVVMWLKDIWKIFDQENREERLRKWM 523
+S K+DV+AFGV+++E+LTG++ A+ ++N K++ + EERL+++MD
Sbjct 523 VSTKLDVYAFGVLMLEILTGEVAAILAEDNN-----KNLSGVLSAVLG-EERLKEFMD 575
Query 524 PKLDNYYPIDYALSASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATLERSLTSSG 582
P L + YP + A+ + + V C SRP++ EIV +LS T S + E S+ SG
Sbjct 576 PSLQSNYPFELAMFVFEIIVGCIKDPASRPSMQEIVPTLS-RTMNSSLSWEMSVNISG 633

```


>dbj|BAI79286.1| LysM type receptor kinase [Lotus japonicus]
Length=633

Score = 267 bits (683), Expect = 3e-69, Method: Compositional matrix adjust.
Identities = 203/659 (30%), Positives = 327/659 (49%), Gaps = 116/659 (17%)

```

Query 1 MAVFFVSLTLGAQILYVVMFFTC-IEAQSQQTNGTNFSCPSNSP-PSCETYVITYISQSP 58
+ +FF AQ Y+ L C S G ++C S +C+ Y+T+ +Q P
Sbjct 14 LFIFFTFPITLAQQPYIGLATNACPRRGNSNSIRG--YTCNGGSANHTCQAYLTFRTQ-P 70
Query 59 NFLSLTSVSNIFDTSPLSIAR----ASNLOHEEDKLIPGVLLIPVTCGTGNRSFANIS 114
+ S+ ++S + + +A + N E +KL+ ++PV C C G AN S
Sbjct 71 IYNSVYTISTLLSSDARHLAETMSVSNQNTTFETNKLV-----IVPVQCSCAGEYYQANTS 125
Query 115 YEINQGDsfYfVATTLYQNLTNWHAVM--DLNPGLSQFTLPIGIQVVIPLFCCKCPKSNQL 172
Y D+ + +A ++ LT A+M + NPG L +G ++ +PL C CP+KNQ
Sbjct 126 YAFQNTDTPFSIANNTFEGLTTCQALMHENHNPg----HLYLGRELTVPLRCACPTKNQT 181
Query 173 DRGKYLITHVWQPNNDNVSVSNKLGASPDILSENNYGNFTAAASNLPVLIPVTLTPDL 232
++GKYL+++ D++S +S K G S + L N+ + T A P TLL L
Sbjct 182 EKGKYLSSLYVNWGDSISVISEKFGVSCNNTLEANS--SLTKAKIYPF---TTLVPL 236
Query 233 IQSPSDGR-----KHRIGLPVIIGISLGCTLLVVVSAILLVC 269
PS+ + ++ L V++G G L+V++A++ C
Sbjct 237 HDKPSNSQTILQSQPSSTSSSPSSSTHQSSNKTWLYVVVG---GVFALIVLTAVIF-C 292
Query 270 VCCLMKSLNRSASSAETAD-----KLLSGVSGYVSKPTMYETGAILEA 313
+ K + + S S ++ KL + G +Y I A
Sbjct 293 IHYHKGRRKDDSLQLTVSESFENQQLGKEMKKGDGKLEFIHGIAQSFKVYSFEEIQRA 352
Query 314 TMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHNGLVLMGVSSDNDG 373
T NL+ I SVY+ + G ++A+K+ + DV++E++IL KVNH N+++L GVS N+G
Sbjct 353 TNNLNSSSLIKGSVYRGVMNGDLVAIKKTEGDVSKETQILKNVHNSNVIRLSGVSF-NEG 411
Query 374 NCFVVEYEAENGSLLEEWLFAKSCSETSNRSTSLTWCQRIISIAVDVSMGLQYMHEHAYPRI 433
++VVEYA NG L EW+F L+W QRI IA+DV++GL Y+H P
Sbjct 412 QWYLVEYEAANGPLSEWIFFGKF-----LSWTQRIQIALDVAIGLDYLHSFTSPPH 462
Query 434 VHRDITSSNILLDSNFKAKIANFSMART-----FTNPM 466
+H+D+ SSNILLDS+FAKIAN S+AR+ N +
Sbjct 463 IHKDLKSSNILLDSDFRAKIANLSLARSVKGVEDDDQFLATRNIVGTRGYMAPEYLENGL 522
Query 467 MS-KIDVFAFGVVLIELLTGRK--AMTTKENGVEVVMWLKDIWKIFDQENREERLRKWM 523
+S K+DV+AFGV+++E+LTG++ A+ ++N K++ + EERL+++MD
Sbjct 523 VSTKLDVYAFGVLMLEILTGEVAAILAEDNN-----KNLSGVLSAVLG-EERLKEFMD 575
Query 524 PKLDNYYPIDYALSASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATLERSLTSSG 582
P L + YP + A+ + + V C SRP++ EIV +LS T S + E S+ SG
Sbjct 576 PSLQSNYPFELAMFVFEIIVGCIKDPASRPSMQEIVPTLS-RTMNSSLSWEMSVNISG 633

```

>ref|XP_002533279.1|  serine-threonine protein kinase, plant-type, putative [Ricinus communis]
gb|EEF29111.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]
Length=617

GENE ID: 8272991 RCOM_0411670 | serine-threonine protein kinase, plant-type, putative [Ricinus communis]


Score = 264 bits (674), Expect = 3e-68, Method: Compositional matrix adjust.
Identities = 179/580 (30%), Positives = 309/580 (53%), Gaps = 74/580 (12%)

```

Query 37 FSCPSNSPPSCETYVITYISQSPNFLSLTSVSNIFDTSPLSIARASNLOHEEDKLIP-GQV 95
++C N SC+T++ Y SQ P + +++S+S + + PL +A +N+ + ++P +
Sbjct 47 YTC--NGKESCKTFLIYKSQPP-YHTVSSISKLTSSDPLELALINNISNF--TVLPNTKE 101
Query 96 LLIPVTCGCTGNRSFANISYEI-NQGDsfYfVATTLYQNLTNWHAVMDLNPGLSQFTLPI 154

```



```
Sbjct 102 +++P+ C C+ AN SY I + D+++ +A + Y+ L+ +++M N S+F+L + 160
VIVPIICSCSSQYQANTSYIIPISIYDIFYSIAESTYEGGLSTCNSLMRQN-NYSEFSLDV
Query 155 GIQVVIPLFCCKPSKNQLDRGIKYLITHVWQPNDNVSVFVSNKLGASPDILSENNYGQNF 214
G+++ +PL C CP+ NQ G KYL+T+ D V VS + AS + NY F
Sbjct 161 GMELRVPLRCACPTSNQSANGTKYLLTYSVSWGDKVRAVSERFNASIDSV----NYANGF 216
Query 215 TAASN--LP---VLIPVTLPLDLIQS-----PSDGRKHRIGLPVI 249
T P +L+P++ P Q+ S + H +PVI
Sbjct 217 TKDDTTLPFTTILVPLSTEPSSFQITIVHYPPPPYSPFFIPVHPIRRSRKKIHVWVPIVI 276
Query 250 IGISLGCTLLVVVSAILLVCCCLMKMSLNRSASSAETADKLLSGVSGYVSKPTMYETGA 309
I +L L +V+ +L L ++ + E D L V+ +Y
Sbjct 277 IVSALPVVLFIVL--LLRNKKSGLGVQREKEGKNKEELPDDFLDHVAHVDLGLKIYTFEE 334
Query 310 ILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHNGLVLMGVSS 369
+ AT + S ++ +SVY+ I G+VLA+K+ +DV+ E+ +L+K+NH NL+ L +
Sbjct 335 LKVATEDFSTSNRLSDSVYRGVISGQVLAIKMSKDVSEVTLRKRINHFNLSLHA-AC 393
Query 370 DNDGNCFFVVEYAENGSLLEEWLFAKSCSETSNRSTSLTWCQRISIAVDVSMGLQYMHEHA 429
++ G +++YE+ +NGSL +WL+ ++C E +W +RI IA+DV+ GL Y+H
Sbjct 394 EHHGVFVLMYEFMDNGSLRDWLYKRNCLEAQ-----SWNRRIQIALDVANGLHYLHNFT 447
Query 430 YPRIVHRDITSSNILLDSNFKAKIANFSMART-----FTNP----- 465
P VH+DI+SSN+LL + +AKIANFS+AR+ + P
Sbjct 448 DPPYVHKDISSNVLLSRHLRAKIANFSLARSAKAEHVNSSLRLALGSKGYLAPEFIDF 507
Query 466 --MMSKIDVFAFGVVLLIELTGRKAMTKENGEVVMWLDIWKIFDQENREERLRKWMMD 523
+ +ID++AFGVVL+EL+TG++A+ +E +V L + I I ++E N E RL +D
Sbjct 508 GLVTFEIDIYAFGVVLELVTGKEAVYMQEERKV-QLSETIISIMEKE-NAEARLGCIVD 565
Query 524 PKLDNYYPIDYALSASLAVNCTADKSLSRPTIAEIVLSL 563
P L + + ++ L + L++ C A + SRP++AEIV +L
Sbjct 566 PNLQSQSHMEVVLRMVKLSLACLAEQEPESRFSMAEIVSAL 605
```

>ref|XP_002533278.1|  BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]
gb|EEF29110.1| BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]
Length=647

GENE ID: 8272990 RCOM_0411660 | BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]

Score = 263 bits (673), Expect = 4e-68, Method: Compositional matrix adjust.
Identities = 187/626 (29%), Positives = 314/626 (50%), Gaps = 95/626 (15%)

```
Query 18 VLMFFTICIEAQSQQ-----TNGTN-----FSCPSNSPPSCETYVITYISQSPNLSL 63
+ + F C+ +QQ TN TN +SC + SC+TY+T+ SQ P + ++
Sbjct 14 IFLAFCCLLIHAQQPYVAKATTNCTNTADSALGYSC-NGLNTSCQTYLTFRSQPP-YTNV 71
Query 64 TSVSNIFDTSPLSIARASNLQHEEDKILPGQVLLIPVTCGCTGNRSFANISYEINQGDSE 123
TS+S + ++ P ++ +A N E +++++PV C C+G+ AN SY + D+
Sbjct 72 TSISTLNSDPSQLS-AINSVSETATFDTNKLVIVPVNCSCSGDYQANTSYVVQAKDAP 130
Query 124 YFVATTLYQNLNWHAVMDLNPGLSQFTLPIGIVVPLFCCKPSKNQLDRGIKYLITHV 183
+FA +Q L+ A+ D N + P I + IPL C CP+KNQ D GIKYL++++
Sbjct 131 FFIANNFFQGLSTCQAINDQNRRTVDIFPNEI-LHIPLRCACPTKNQTDAGIKYLLSYL 189
Query 184 WQPDNVSVFVSNKLGASPDILSENNG-QNFTAASNLPVLIPVTLPLDLIQS----- 235
D VS VS K G + L N Q T +LIP+ P Q+
Sbjct 190 VTWGDVTSVAVSVKFGGNTGRSLEANGLSEQTPTIYPFTTLLIPIENPPTSNTISPPPPP 249
Query 236 -----PSDGRKHRIGLPVIIGISLGCTLLVVVSAILLVCC----- 272
P++G + + V+G+ G + + I+ +
Sbjct 250 ASSPPPPSTDTPNNGSSKKWVYVLVGVLAGIVFTLGLVTIIFYALFRRSRKRKPEPIIV 309
Query 273 -----LKMMSLNRSASSAETADKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESV 327
+ KSLN+ E + L +S +Y+ + AT N S C I SV
Sbjct 310 SESFEAQEKSLSNKKLD--EESQDFLDSISSIAQSIKVKFKELEAATDNFSPSCWIKGSV 367
Query 328 YKANIEGKVLAVKRFKEDVTEELKILQKVNHNGLVLMGVSSDNDGNCFFVVEYAENGSL 387
Y+ I G A+K+ DV++E++L KVNH NL++L GV G+ ++VVEYA NG+L
Sbjct 368 YRGYISGDYAAIKKVGNDVSKEIELLNKVNHNFLIRLSGVCFSG-GHWYLVVEYAANGAL 426
Query 388 EEWLFAKSCSETSNRSTSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDS 447
+W++ ++N L+W QR+ IA+DV+ GL Y+H P +H+DI SSN+L+DS
Sbjct 427 SDWYY-----SNNEGFLSWTQRVQIALDVATGLNLYHSFTSPPHHKDIKSSNVLIDS 481
Query 448 NFKAKIANFSMART-----FTNPMS-KIDVFAFGVVLLIE 481
+F+AKIAN +MAR+ N ++S K+DV+AFG++++E
Sbjct 482 DFRAKIANLAMARSTEGQDGEFALTRHIVGTYKGYMAPEYLENGLVSTKLDVYAFGIMLE 541
Query 482 LLTGRK--AMTKENGEVVMWLDIWKIFDQENREERLRKWMDPKLDNYYPIDYALSLSA 539
++TG++ A+ T+EN + + D+ +E+ ++ L++++DP ++ +P +L +
Sbjct 542 MVTGKEVAALYTEENLNLSLILNDVLS----KEDGQQLKQFVDPSEENFPSEISLFMM 597
Query 540 SLAVN-CTADKSLSRPTIAEIVLSL 564
++ C RP + EI SLS
Sbjct 598 VRMIDSLCNKNPADRPAMDEISQSL 623
```

>ref|XP_002522569.1|  BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]
gb|EEF39869.1|  BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]
Length=624

GENE ID: 8259229 RCOM_1014860 | BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]

Score = 262 bits (669), Expect = 1e-67, Method: Compositional matrix adjust.
Identities = 180/601 (29%), Positives = 304/601 (50%), Gaps = 69/601 (11%)

```
Query 25 IEAQSQTNGTNFSCPSNSPP-----SCETYVITYISQSPNLSLTSVSNIFDTS 73
```


9/27/2010

Length=637

GENE ID: 8260932 RCOM 1593420 | serine-threonine protein kinase, plant-type, putative [Ricinus communis]

Score = 258 bits (658), Expect = 2e-66, Method: Compositional matrix adjust.
Identities = 164/557 (29%), Positives = 164/557 (29%), Gaps = 53/557 (9%)


Query	46	SCETYVYIYISQSPNFLSLTSVSNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCT	105
		+C+ ++ + S+ P + S ++S + S +AR +N+ + + +V+ +PV+C C	
Sbjct	54	TCQAFILFRSRPP-YDSAPTISALTSASQEELARFNNVTGLSEFPLNKEVI-VPVSCSCL	111
Query	106	GNRSFANISYEINQGDSEFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCK	165
		G AN S+++ S++ +A+ Y+ L+ ++ N +F L +G ++ +PL C	
Sbjct	112	GQYYQANTSFQVADSHSYFTIASQTYEGLSTCASLKKANI-YGEFDLALGAEQVPLRCA	170
Query	166	CPSKNQLDRGIKYLITHVWPNDNVSVSNKLGASPDILSENNGQNFATAASNLPVLIP	225
		CP+ +Q+ KYL+T +D+++ ++ + S + I+ N ++ T + +LIP	
Sbjct	171	CPTASQVRNETKYLTLTFPISESDHIAAIAERFNVSKESIIDANGLRESPTIYPDTTILIP	230
Query	226	VTLLPDLIQS-----SPSDGRKHRIGLPVIGISLGCTLLVWVSAILLVCV	270
		+T P Q SP D R+ + L +GI+ C+LLV+ +I++V +	
Sbjct	231	LTTEPSNSQTIIHENPTEVSPPLASPPDNRRSKRKLYEKGITAACSLVL--SIIIVVIL	288
Query	271	CCLKMKSLNR--SASSAETADKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVY	328
		L+ ++ + L ++ ++ +AT N S + I S+Y	
Sbjct	289	FLLRKDRRRHKFPEINRRREQEDLRLEIASVEQVLKVFGLVEVKKATDNFSSKHIKGSly	348
Query	329	KANIEGKVLAVKRFKEDVTEELKILQKVNHGKLVKMGVSSDNDGNCFFVVEYAENGSL	388
		G++LA+K+ DV++E+ IL++NH NL+KL GV +N G ++ +EY +NGSL+	
Sbjct	349	WGEFNGQILAIAKMMNRDVSKEVNILKRINHFNLIKHLGVC-ENLGCIFYLFFEYMKNGSLQ	407
Query	389	EWLFAKSCSETSNRSTSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSN	448
		EWL + + +W QRI IA+D++ GL Y+H P VH+DITS +ILLD+N	
Sbjct	408	EWLSRERFEDVG-----SWNQRIQIALDIANGLFYLSFTEPACVHKDITSGHILLDNN	461
Query	449	FKAKIANFSMARTFTNPMMS-----KIDVFAFGVVLIELLTGR	486
		+AKIANFS+AR N +++ KIDV+AFG+VL+EL+TG+	
Sbjct	462	LRAKIANFSLARAAANAVLTKHIEGTRGYMAPEYVQAGQVTPKIDVYAFGIVLELITGK	521
Query	487	KAMTTKENGENVMLWKDIWKIFDQEEENREERLRKWMDPKLDNYYPIDYALSLASLAVNCT	546
		A+ ++ G+ +L K I+ + ++ EN E L +DP AL LA +++ C	
Sbjct	522	DAVFMRD-GKETLLSKAIFSVMEK-ENAEAEALAFVIDPSFTGGRQSKLALRLARVSLACL	579
Query	547	ADKSLSRPTIAEIVLSL 563	
		RP++ E+V +L	
Sbjct	580	TQVPARRPMSGVEVVSTL 596	

>ref|XP_002269408.1|  PREDICTED: hypothetical protein [Vitis vinifera]
Length=638

GENE ID: 100242712 LOC100242712 | hypothetical protein LOC100242712 [Vitis vinifera]

Score = 256 bits (653), Expect = 9e-66, Method: Compositional matrix adjust.
Identities = 171/574 (29%), Positives = 292/574 (50%), Gaps = 66/574 (11%)

Query	46	SCETYVYIYISQSPNFLSLTSVSNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCT	105
		SC+ ++ + S+ P + ++S+S++ + P +A+ +++ E + + ++PV C C+	
Sbjct	54	SCQAFILFRSEPP-YNDVSSISDLLGSDPSQLAINSVD-ETATFETKKEVIVPVNCS	111
Query	106	GNRSFANISYEINQGDSEFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCK	165
		G S AN SY + GD++ +A ++ L+ A+ L+ + G ++ +PL C	
Sbjct	112	GEFSQANTSVVQHGDTYLLIANNTFEGSLSTCQALRSQRTSLTT-NIYTGKLTVPPLRCA	170
Query	166	CPSKNQLDRGIKYLITHVWPNDNVSVSNKLGASPDILSENNGQNFATAASNLPVLI	224
		CP+KNQ D G+KYL++++ D VS +S + G L N QN +LI	
Sbjct	171	CPTKNQSDVGVKYLMSYLVASGDYVSSISVRFVDTGMTLEANELSEQNPNIYPFTTLLI	230
Query	225	PVTLLPDLIQS-----PSDGRKHRIGLPVIGISLGCTLLVWVSAILL	266
		P+ LP Q+ + + V++G+ G L+++ ++	
Sbjct	231	PLQNLPSSSQTIVPPPPPPPPPTAVSSPSKSLKKTWVYVVGGVVAGSALVLLFGSVI	290
Query	267	LVCVCLKMKSLNRSASS-----AETADKLLSGVSGYVSKPTMYETGAILEATMN	316
		K + A S E + L +S +Y+ + AT N	
Sbjct	291	FFKFFRKRTRKTDPIAISESEFEACEKPLKEEQHEFLESISSIAQSLKVYKFEELQSATDN	350
Query	317	LSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGKLVKMGVSSDNDGNC	376
		S C+I SVY+ I+G + A+K+ +V+ E+ +L K+NH N+++L G+ NDG+ +	
Sbjct	351	FSPNCRKSGSVYRGITIKGDLAAIKKMDGEVSNEIALLNKINHFNVIRLSGICF-NDGHWY	409
Query	377	VVEYAENGSLLEWLFAKSCSETSNRSTSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHR	436
		+V+EYA NG L +W++ + +SR L W QRI IA+DV+ GL Y+H + P VH+	
Sbjct	410	LVHEYAVNGPLTDWIY----NNNDDSRF-LVWMQRIQIALDVATGLNYLHSYTPPYVHK	464
Query	437	DITSSNILLDSNFKAKIANFSMART-----FTNPMMS-KI	470
		DI S N+LLDS+F+AKIANF +AR+ N ++S K+	
Sbjct	465	DIKSGNVLLSDFRKIANFGLARSAGQEGQFALTRHIIGTRGYMAPEYLEGLVSTKL	524
Query	471	DVFAFGVVLIELLTGRKAMTTKENGENVMLWKDIWKIFDQEEENREERLRKWMDPKLDNY	530
		DV+AFGV++E+LFG++ E GE + L D+ E + +E+LR ++DP L Y	
Sbjct	525	DVYAFGLVLMLEMTGKEVAALYE-GENMHL-PDVLVAVLHEGDGKEKLRNFIDPSLSGNY	582
Query	531	PIDYALSLASLAVNCTADKSLSRPTIAEIVLSL 564	
		P++ A+ + L +C SRP + EIV +LS	
Sbjct	583	PLELAIVMIRLIDSLCKKSPASRPDMVEIVQALS 616	

>ref|XP_002281880.1|  PREDICTED: hypothetical protein [Vitis vinifera]
Length=622

GENE ID: 100248852 LOC100248852 | hypothetical protein LOC100248852 [Vitis vinifera]

Score = 254 bits (650), Expect = 2e-65, Method: Compositional matrix adjust.
Identities = 188/608 (30%), Positives = 305/608 (50%), Gaps = 83/608 (13%)

```

Query 23 TCIEAQSQQTNGTNFSCPS--NSPPS-----CETYVITYISQSPNFLSLTSVS 67
+CI AQ + + + +C + +S PS C + + + S+ P + S+ ++S
Sbjct 16 SCINAQQEYSGNSVLNCDNSDDSGPSSAFLYTCNGLYSSCQAFILFKSEPP-YNSVPTIS 74

Query 68 NIFDTSPLSIARASNLOHEEDKLIP-GQVLLIPVTCGCTGNRSFANISYEINQGSFYFV 126
+ ++P +AR ++++ + P G+ +++PV C C G AN ++ I YF+
Sbjct 75 MLMSSNPGEARINSVK--TLTVFPTGKEVIVPVNCSCLGQYYQANTTFHIQDNQQTYYFI 132

Query 127 -ATTLYQNLTNWHAVMDLNPGLSQFTLPIGIVQVVIPLFCKCPSKNQLDRLGIKYLITHVWQ 185
YQ L+ ++M N S+F+L G+++ +PL C C +++Q + G KYL+T+
Sbjct 133 IGNNTYQGLSTCDSLMRAN-RYSEFSLSPGLELHVPLRCACHEHQAENGTKYLLTYSVS 191

Query 186 PNDNVSFVSNKLGASPDILSENYY--GQNFTAASNLPVLIPTLLPDLIQ----- 234
DN + + + S + I N +N T +LIP+ P Q
Sbjct 192 WEDNFPPTIGERFNVSAKSIADANGLISEENPTIFFPFTTILIPKTEPLSSQTKTHATQPV 251

Query 235 -----SPSDGRKHRIGLPVIIGISLGCTLL---VVVSAILLVCCCLMKMSLNRSA 282
S S K RI L G I+ GC LL V+ S + L K
Sbjct 252 LDPPPPPTSDSGSSRSKRRIYLG--GIAAGCFLLGPSVIFSVIFLYKKRSKKVPPVHGK 309

Query 283 SSAETADKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRF 342
+ + + LL ++ P ++E + +AT N S + +I V++A + +++AVK+
Sbjct 310 TKSVLPEDDLVEIASVDPVPKVFEEFKLKKATGNFSSKSRIKGCVFRAELGREIVAVKKM 369

Query 343 KEDVTEELKILQKVNHNVLKLMGVSSDNDGNCF-VVVEYAENGSLLEEWLFAKSCSETSN 401
K D+EE+ IL K+NH NL+KL GV +G+CF +V+EY ENGSL EWL +S
Sbjct 370 KVDISEEVNILNKLHNCLIKLHGVC--KNGSCFYLVFEYMENGSLREWLHKES----- 421

Query 402 SRTSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMART 461
S S +W +RI IA+DV+ GL Y+H P VH+ I SSNILL N +AKIANFS+ART
Sbjct 422 SNHSQSSWSKRIQIALDVANGLHYIHNFTKPAYVHKHKSSNILLTKNLRAKIANFSLART 481


Query 462 -----FTNP-----MMSKIDVFAFGVVLIELLTGRKAMTTKENG 495
+ P + K+DV+AFGVV++EL+TG+ A+ +N
Sbjct 482 AVKGAKTHALNMLVVGTRGYMAPEYIEAGSITPKVDVYAFGVVMLEITGKDAVII-QNE 540

Query 496 EVVMLWKDIWKIFDQENREERLRKWMDPKLDNYYPIDYALSASLAVNCTADKSLSRPT 555
E V+L + + I ++ N E L ++DP L I + A +A L++ C RP+
Sbjct 541 EEVLSEAMISIMER-GNAEIELGHFLDPCLLGNGGIESATRIAKLSIACLTQDQARRPS 599

Query 556 IAEIVLSL 563
+ E+V +L
Sbjct 600 MGEVVSTL 607

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>ref|XP_002310777.1|  predicted protein [Populus trichocarpa]

gb|EEE91227.1|  predicted protein [Populus trichocarpa]
Length=643

GENE ID: 7477999 POPTRDRAFT_563086 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score = 253 bits (645), Expect = 6e-65, Method: Compositional matrix adjust.
Identities = 179/585 (30%), Positives = 280/585 (47%), Gaps = 82/585 (14%)

```

Query 46 SCETYVITYISQSPNFLSLTSVSNIFDTSPLSIARASNLOHEEDKLIPGQVLLIPVTCGCT 105
SC+ Y+ + SQ P + ++ S+S + + P +++ +++ E Q++L+PV C C+
Sbjct 53 SCQAYLIFRSQPP-YSTVASISTLLGSDPSQLSQINSVS-ETTSFPTNQLVLPVNCSCS 110

Query 106 GNRSFANISYEINQGSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIVQVVIPLFCK 165
G+ + AN SY + G++ + +A YQ L+ A+ + G + G + +PL C
Sbjct 111 GDYFQANASYIVQSGNTPFLIANNITYQGLSTCQAIRN-EKGRTRTVNIFAGETLTVPLRCA 169

Query 166 CPSKNQLDRLGIKYLITHVWPNDNVSFVSNKLGASPDILSENYYGQ-NFTAASNLPVLI 224
CP+KNQ D GI+YL++++ D VS + GA L N + N T +LI
Sbjct 170 CPTKNQSDLGIRYLLSYLVWTGDTVSIAGVRFGADIGRALEANEISEKNPTIYFPTLLI 229

Query 225 PVTLLPDLIQS-----PSDGRKHRIGLPVIIGISLGCTLLVVVSAI 265
P+ P Q+ SD ++ + V +G G L +V+ I
Sbjct 230 PLKNPPTSSQTTVVPPPPASPSPSPSPSNSDKSANKTWIYVFGAVGGIVLTLVIGTI 289

Query 266 LLVCVCCCLMKK-----LNRSAASAEADKLLSGVSGYVSKPTMYETGA 309
+ + K LNR E LL V +Y
Sbjct 290 IFFMLFRKSKQPGPIIVSQSFEAHEKPLNRKLD--EEPQDLLESVYSIAQSIKVVNYED 347

Query 310 ILEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHNVLKLMGVSS 369
+ AT N S I SV++ I G A+K+ DV++E+ +L K+NH NL++L GV
Sbjct 348 LKAATDNFSPSPFWIKGSVFRGLINGDFAAIKKMNGDVSKEIDLNNKINHNSNLIRLSGVCF 407

Query 370 DNDGNCFVVVEYAENGSLLEEWLFAKSCSETSNRSTLTWCQRISIAVDVSMGLQYMHEHA 429
NDG+ ++VVEYA NG L +W++ +SN L W QRI IA DV+ GL Y+H
Sbjct 408 -NDGHWLVVEYAANGPLSDWIYV----SSNEGKFLKWTQRIQIATDVATGLNYLHSFT 461

Query 430 -YPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNP----- 465
YP VH+DI SSNILLD + +AKIANFS+AR+ P
Sbjct 462 NYPH-VHKDKSSNILLDKDLRAKIANFSLARSTDGPEGEFALTRHIVGTGKGYMAPEYLE 520

Query 466 ---MMSKIDVFAFGVVLIELLTGRK--AMTTKENG EVVMLWKDIWK-IFDQENREERLR 519
+ +K+DV+AFG++ +E++TG++ A+ +EN E+ D+ + +E EE L
Sbjct 521 NGIICKLDVYAFGILTLEIMTGKEVAALYREENREL----SDVLNGVLSEEGGLEESLS 576

Query 520 KWMDPKLDNYYPIDYALSASLAVNCTADKSLSRPTIAEIVLSLS 564
+ +DP + YP A+ + L +C RP + EIV SLS
Sbjct 577 QLIDPSMQGNYPGLAVLMVRLIDSCLNKNPAGRPAMDEIVQSLS 621

```

>gb|ABQ59612.1| LYK4 [Glycine max]
Length=633

Score = 253 bits (645), Expect = 8e-65, Method: Compositional matrix adjust.
Identities = 191/629 (30%), Positives = 322/629 (51%), Gaps = 77/629 (12%)

```

Query 7 SLTLGAQILYVVMFFTCIEAQSQQTNGTNFSCPSNSPPSCETYVITYISQSPNFLSLTSV 66
SL LG Q Y+ L C + + + +C + + SC++Y+T+ SQ P + S+ ++
Sbjct 20 SLILGQQP-YIRGLTVAC-PRRGKNKSIRGYTC-NGANHSCQSYLTFRSQ-PIYNSVKTI 75

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```
Query 67 SNIFDTSPLSIARASNQHEEDKLIPQVLLIPVTCGCTGNRSFANISYEINQGDSFYFV 126
S + + P +A+ +++ D +++++PV C C G N SYE + +++ +
Sbjct 76 STLLGSDPSQLAKINVSVMN-DTFETNKLIVIPVNCSCAGEYYQTNTSYEFHNSETYFLI 134

Query 127 ATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHVWQP 186
A ++ LT A+ + N + P G +++PL C CP+KNQ ++GI+YL+++
Sbjct 135 ANNTFEGLTTCQALENQNHNPANI-YP-GRLLVPLRCACPTKNQTEKGIRYLLSYLVNW 192

Query 187 NDNVSFVSNKLGASPDILSENNYQGNFTAASNLP---VLIPVTLPLDLIQSPSDGRKHR 243
D+VSF+S K G + L N T A+ P +L+P+ P Q+ S R+
Sbjct 193 GDSVSFISEKFGVNFMTTLEANTL--TLTQATIYPFTTILVPLHDKPSSSQTVSPTRRTP 250

Query 244 IGLPVIIGISLGTCT----LLVVVSAILLVCCVCC-----LKMKSLN 279
P S T + VVV AI L+ V C + KS
Sbjct 251 PPSPPSSDHSSNKTWVYVVGVVGAIALISVLCVIFFTRYRKNRKKDDSVVVGSKSFE 310

Query 280 RSASSAETA--DKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKIGESVYKANIEGKVL 337
E +KL +SG +Y + AT N S I SVY+ I G +
Sbjct 311 AIEEKPEVKVNEKLESEIISGIAQSFKVYNFEELQRAITDNFSPSSWIKGSVYRGVINGDLA 370

Query 338 AVKRFKEDVTEELKILQKVNHGNLVKLMGVSSDNDGNCFFVVEYAENGSLLEWLFKSCS 397
A+KR + DV++E++IL K+NH N+++L GVS ++G ++VVEYA NG L EW++ + +
Sbjct 371 AIKRIEGDVSKETIILNKINHSNVIRLSGVSF-HEGGWYLVVEYAANGDLSEWIYFHNVN 429


Query 398 ETSNSRTSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFS 457
L+W QR+ IA+DV+ GL Y+H P +H+DI SSNILLD +F+ K+ N S
Sbjct 430 -----GKFLSWTQRMQIALDVATGLDYLHSFTSPPHIHKDINSSNILLDGFGRKVTNLS 484

Query 458 MARTFT-----NPMMS-KIDVFAFGVVLIELLTGRK--AM 489
+AR N ++S K+DV+AFGV+++E++TG++ A+
Sbjct 485 LARCLEGGDDQLPATRHIVGTRGYMAPEYLENGLVSTKLDVYAFGVLMLEMTGKEVA AI 544

Query 490 TTKENGEVVMLWKDIWKIFDQEEENREERLRKWMDPKLDNYYPIDYALSLASLAVNCTADK 549
T++ ++ + I EE+ +E L+++DP L P++ A+ + + NC
Sbjct 545 LTEDETKLSHVLSGILG----EESGKEMLKEFVDPSPSGENCPLLEAMFVIEMIDNCIKTD 600

Query 550 SLSRPTIAEIVLSLSLLTQSPATLERSL 578
SRP++ EIV S+S T S + ERS+
Sbjct 601 PASRPSVHEIVQSMS-RTLKSSLSWERSM 628
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>ref|XP_002327712.1|  predicted protein [Populus trichocarpa]

gb|EEE75190.1|  predicted protein [Populus trichocarpa]
Length=630

GENE ID: 7464252 POPTRDRAFT_796841 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score = 249 bits (635), Expect = 9e-64, Method: Compositional matrix adjust.
Identities = 178/583 (30%), Positives = 290/583 (49%), Gaps = 80/583 (13%)

```
Query 46 SCETYVTVYISQSPNFLSLTSVSNIFDTSPLSIARASNQHEEDKLIPQVLLIPVTCGCT 105
SC+ Y+ + SQ P + ++ S+S + + P ++ +++ E Q++++PV C C+
Sbjct 42 SCQAYLIFRSQPP-YNTVASISTLLGSDPSQLSEVNSVS-ETTSFSPSNQLVIVPVNCS 99

Query 106 GNRSFANISYEINQGDSFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCK 165
G S AN SY + D+ + +A YQ L+ A+ + + L G + +PL C
Sbjct 100 GEYSQANASYIVQPNDFLFIANNNTYQGLSTCQALQNQKTRTRTDDILS-GETLTVPLRCA 158

Query 166 CPSKNQLDRGIKYLITHVWQPNNDVSVSNKLGASPDILSENNY-QGNFTAASNLPVLI 224
CP+KNQ D GI+YL+++ P D+V +S +GA+ L N QN T +LI
Sbjct 159 CPTKNQSDLGIRYLLSYLVTFGDDVPAISEQFGAATGRTLEANGLPEQNPTIFPFTLLI 218

Query 225 PVTLLPDLIQS-----PSDGRKHRIGLPVIIGISLGTCTLLVVVSAILL 267
P+ P Q+ + + + L V++G+ G L +V+ I+
Sbjct 219 PLQSTPTSSQTVPVPPPPPPASSPPSPSPNPEKSSKKTWLYVVVGVGIALTIVIGTIIF 278

Query 268 VCVCCCLKMS-----LNRSASSAETADKLLSGVSGYVSKPTMYETGAIL 311
+ K LN+ E + + +S +Y+ +
Sbjct 279 FMLSRKSKKPGPVIESQSFEAHEKPLNKKLD--EESQEFFESISATAQSIKVKYFEDLK 336

Query 312 EATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNLVKLMGVSSDN 371
AT N S C I SVY+ I G A+K+ DV++E+++L K+NH NL++L GV N
Sbjct 337 AATDNFSPSCWIKGSVYRGLINGDFAAIKKMNGDVSKEIELLNKINHSNLRILSGVCF-N 395


Query 372 DGNCFFVVEYAENGSLLEWLFKSCSETSNRSTSLTWCQRISIAVDVSMGLQYMHEHA-Y 430
DG+ ++VVEYA +G L +W++ +S N L W +RI IA DV+ GL Y+H Y
Sbjct 396 DGHWYLVVEYAASQGLSDWIYDRS----NEGKFLNWKRIQIASDVATGLNLYHSFTNY 450


Query 431 PRIVHRDITSSNILLDSNFKAKIANFSMART-----FTNP----- 465
P VH+DI SSNILLDS+ +AKIANFS+AR+ + P
Sbjct 451 PH-VHKDIKSSNILLDSDLRAKIANFSLARSTGDQDDEFVLTRHIVGTRGYMAPEYLENG 509


Query 466 -MMSKIDVFAFGVVLIELLTGRK--AMTTKENGEVVMLWKDIWK-IPDQEEENREERLRKW 521
+ SK+DV+AFG++ +E++TG++ A+ ++E+ + D+ + + +EE L++
Sbjct 510 WVSSKLDVYAFGLTLEIITGKEVAALHSESRNL---SDVLNGALSEVDGQEEESLKQL 565


Query 522 MDPKLDNYYPIDYALSLASLAVNCTADKLSRPTIAEIVLSLS 564
+DP L YP A+ + L +C RPT+ EIV SLS
Sbjct 566 IDPSLHENYPSGLAVLVVRLIDSLNKNPGRPTMDEIVQSLS 608
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>ref|NP_001058110.1|  Os06g0625200 [Oryza sativa Japonica Group]

dbj|BAD35689.1|  receptor protein kinase-like [Oryza sativa Japonica Group]

dbj|BAD37734.1|  receptor protein kinase-like [Oryza sativa Japonica Group]

dbj|BAF20024.1|  Os06g0625200 [Oryza sativa Japonica Group]


gb|EAAZ37689.1|  hypothetical protein OsJ_22029 [Oryza sativa Japonica Group]
Length=630

GENE ID: 4341567 Os06g0625200 | Os06g0625200 [Oryza sativa Japonica Group]
(10 or fewer PubMed links)

Score = 242 bits (618), Expect = 8e-62, Method: Compositional matrix adjust.

Identities = 171/568 (30%), Positives = 291/568 (51%), Gaps = 66/568 (11%)

Query	46	SCETYVTVYISQSPNFLSLTSVSNIFDTSPLSIARASNQHEEDKLIPGQVLLIPVTCGCT	105
		SC Y+T+ S P SV+ + + +P +A A+++ + Q+LL+PV C C	
Sbjct	56	SCTAYLTFRSDPP-----LSVAYLLNATPSAVAAANSVPLAVSPVDGTQLLLVPVPCSC-	109
Query	106	GNRSFA----NISYEINQGDSEFYFVATTLYQNLNWHAVMDLNPGLSQFTLPIGIQVVI	161
		NR+ N +Y I + D+F+ +A +Q LT + +++ NP + I + +P	
Sbjct	110	-NRATGYQHNTTYAIQELDTFFLIANNTFQGLTTYQSIANNPASEAMSPVINGPLAVP	168
Query	162	LFCKCPSKNQLDRIKYLITHVWQPNNDVSVFVSNKLGASPDILSENNGQNFTAASNLP	221
		L C CPS I L+T+V Q DNV+ ++ + ++ D+L+ N	
Sbjct	169	LRACAPSATTTGR--INNLLTYVVQEGDNVTSIARRFNSTHGDVLAANTLLVPLVHPHSHR	226
Query	222	VLIPVTLTPDLIQSPSDGRKHRI-----GLPVIIGISLGCTL--LVVVSAILLVCVCL	273
		V++ T + +P + +K + GL +GI +GC + V A+ L+	
Sbjct	227	VVLANTTITS--TTPPESQKFYVSSPCSNGLLAGLGIGVCGVSAWAALVAVFLLWRRRR	284
Query	274	KMKSLNRSASSAETADKLLSGVSGYVSKPTMYETGAILEATMNLSEQCKI--GESVYKAN	331
		+ S + ET L++ V G V Y I AT +E+ ++ G SVY+A	
Sbjct	285	RRPVGDSGSGMARET--PLVAAVRGAVETLAAYSADIETATAGFAEERRVAAGSSVYRAV	342
Query	332	IEGKVLAVKRKF---EDVTEELKILQKVNHNGLVKMGVSSDNDGNCFFVVEYAENGSL	388
		I G+ AVKR +DV E+ +L +VNH LV+L G+ ++ D + +V E+AENG+L	
Sbjct	343	INGEAFAVKRVAAAGGDDVRGEVDVLGRVNHSGLVRLRGLCANGD-DTYLVLEFAENGALS	401
Query	389	EWLFAKSCSETSNRSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSN	448
		EWL S + R L W QR+ +A+DV+ GL Y+H P VH+++ S N+LLD+N	
Sbjct	402	EWLHPGSAACCL--RRVLGWKQRVLVALDVAGGLNYLHHFTNPPYVHKNLNSGNVLLDAN	459
Query	449	FKAKIANFSMA-----RTFTNP-----MMSKIDVFAFGV	477
		+AK+++ A +P + K+DVF+FGV	
Sbjct	460	LRAKVSSSLGFAVAVAVAAGDDSIALMTHHVVGTHGYLAPEYLEHGLISPKLDVFSFGV	519
Query	478	VLIPELLTGR-KAMTTKENGVEVMLWKDIWKIFDQEEENREERLRKWMDPKLDNYYPIDYAL	536
		+ +ELL+G+ A T ++G+ ++LW+ + D + +LR +MDP+L +YPI A	
Sbjct	520	IQLELLSGKTAATVDDDDGQNMLLWQAADGLVDG-DGAWFKLRAFMDPQLQGHYPIGVAS	578
Query	537	SLASLAVNCTADKSLSRPTIAEIVLSLS	564
		++A+LAV C A + +RP++ E+ ++LS	
Sbjct	579	AVAAALAVRCVAREPRARPSMEEVFVTL	606

>ref|XP_002307830.1|  predicted protein [Populus trichocarpa]

gb|EEE94826.1|  predicted protein [Populus trichocarpa]

Length=659

GENE ID: 7479122 POPTRDRAFT_862283 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score = 239 bits (611), Expect = 7e-61, Method: Compositional matrix adjust.
Identities = 170/591 (28%), Positives = 290/591 (49%), Gaps = 86/591 (14%)



Query	46	SCETYVTVYISQSP-NFLSLTSVSNIFDTSPLSIARASNQHEEDKLIPGQVLLIPVTCGC	104
		SC++Y+T+ S P N L + S IA +NL + + +++PV C C	
Sbjct	58	SCQSYLTFRSMPPYNSPVLIAYLLGVQPSATRIASINNLSSTATIPTNTQVVVPVNCSC	117
Query	105	TGNRSFA-NISYEI-NQGDSEFYFVATTLYQNLNWHAVMDLNPGLSQFTLPIGIQVVIPL	162
		+ + N +Y+++ ++ +++ VA YQ LT ++M NP L +G+ + IPL	
Sbjct	118	YARQYYQHNTSYQLKDKSETYFVSANNTYQGLTTCQSLMSQNP-YGDRNLSLGLTLQIPL	176
Query	163	FCCKPSKNQLDRIKYLITHVWQPNNDVSVFVSNKLGASPDILSENNGQNFTAASNLPV	222
		C CP+ NQ GI +L+T++ D++S ++ G Q +L N P+	
Sbjct	177	RCACPTSNQNASGINHLLTYMVTWGDSSISIAQLFGVDKQRVLDANKLSSSNIIFFPTPI	236
Query	223	LIPVTLTPDLI-----QSPS-----DGRKHRIQLPVIIGISLGCTLLVVVSA	264
		L+P+ P I Q+P+ H+ + +G+ +G L+++ A	
Sbjct	237	LVLPTEPTKIEQPSAAPPAPSPQTPNVSVGGSSDHK---ALYVGVGIGAAFLILLFA	293
Query	265	ILLVCVCLMKMKS LNRSASSAETADKLLSGVSGYVSKP-----T	303
		K + + S++E + L S + + P T	
Sbjct	294	AFGFLFWHRKSRKQKQKPVSTSE-PETLPSVSTDFTVLPVSNKKSWSLSSHDARYAIESLT	352
Query	304	MYETGAILEATMNLSEQCKIGESVYKANIEGKVLAVKRKFEDVTEELKILQKVNHNGLVK	363
		+Y+ + AT ++ I SVY+ + +G AVK K DV+ E+ IL+ +NH N+++	
Sbjct	353	VYKYEDLQVATGYFAQANLIKGSVYRGSFKGDTAAVKKVVKGDVSEINILKMINHNSVIR	412
Query	364	IMGVSSDNDGNCFFVVEYAENGSL EEWLFAKSCSETSNRSLTWCQRISIAVDVSMGLQ	423
		L G ++GN ++VVEYA+NGSL +WL ++N L W QR+ IA DV+ L	
Sbjct	413	LSGFCL-HEGNTYLVEYADNGSLTDWL-----HSNNIYRILAWKQRVRIAYDVADALN	465
Query	424	YMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNP-----	465
		Y+H + P +H+++ +SNILLD+N +AK+ANF +ART N	
Sbjct	466	YLHNYTNPSTYHKNLKTSNILLDANLRAKVANFGLARTLENGQDGLQLTRHVVGTOGYL	525
Query	466	-----MMSKIDVFAFGVVLIELLTGRKAMTT---KENGVEVMLWKDIWKIFDQEEEN	513
		+ K+DVFAFGVV++ELL+G++A T K G+ +L I ++ + +N	
Sbjct	526	APEYIENGVTITPKLDVFAFGVVMLELLSGKEAATAIDKIAGD-DLLSVMIMRVL-EGDN	583
Query	514	REERLRKWMDPKLDNYYPIDYALSASLAVNCTADKSLSRPTIAEIVLSLS	564
		E+L ++DP L + YP+D A S+A LA +C +RP++ ++ + LS	
Sbjct	584	VREKLSAFLDPCLRDEYPLDLAFSMAQLAKSCVEHDLNTRFSMPQVFMMLS	634

>emb|CA002961.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
Length=131

Score = 238 bits (606), Expect = 2e-60, Method: Composition-based stats.
Identities = 109/130 (83%), Positives = 120/130 (92%), Gaps = 0/130 (0%)

Query	411	RISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMSKI	470
		RI+IA+DV++GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART TN MM KI	
Sbjct	1	RIITAMDAIGLQYMHEHTYFRIIHRDITTSNILLGSGNFKAKIANFGMARTSTNSMMFKI	60
Query	471	DVFAFGVVLIELLTGRKAMTTKENGVEVMLWKDIWKIFDQEEENREERLRKWMDPKLDNYY	530
		DVFAFGVVLIELLTG+KAMTTKENGVEV+LWKD WKIFD E NREERLRKWMDPKLD+++Y	



Sbjct 61 DVFAFGVVLIELLTGKKAMTTKENGVEVILWKDFWKIFDLEGNREERLRKWMDFKLESFY 120
 Query 531 PIDYALSLAS 540
 PID ALSLAS
 Sbjct 121 PIDNALSLAS 130

>ref|XP_002509540.1|  ATP binding protein, putative [Ricinus communis]
 gb|EEF50927.1|  ATP binding protein, putative [Ricinus communis]
 Length=681

GENE ID: 8271475 RCOM_1677900 | ATP binding protein, putative
 [Ricinus communis]

Score = 236 bits (602), Expect = 7e-60, Method: Compositional matrix adjust.
 Identities = 192/638 (30%), Positives = 304/638 (47%), Gaps = 101/638 (15%)

Query 25 IEAQSQQTNGTNTFSCPSN-SPSCETYVTYISQSPNFLSLTSVSNIFDTSPLSIARASNL 83
 + ++ + + + C N S C+T+ +S + F SL+++S + IA A+
 Sbjct 30 LSCETTSPDASGYRCNINGSQDHCKTFAI-LSTNSYFSSLSNLSFYLGFRNFVIAEANGF 88
 Query 84 QHEEDKILIPGQVLLIPVTCGCTGNRSFANISYEINQGDSFYFVATTLYQNLTNWHAVM 143
 + + L Q LLIP+ C C GN A ++ +G++FY +A +L + LT A+ +
 Sbjct 89 SATTEFLPKDQPLLPIDCKCNGNFFRAEVTKTTIKGENFYGIAESL-EGLTTCKAIQEN 147
 Query 144 NPGLSQFTPLPIGIQVVIPLFCCKPSKNQLDRGIKYLITHVWQPNNDNVSFVSNKLGASPD 203
 N G+S + L ++++PL C CPS +Q+ ++L+++ D +S ++ K +P+
 Sbjct 148 NLGVSPWNLDADKARLLVPLRCACPFSSSQVTLATRFLLSYFPVSEGDITISNIAIKFNTTPEA 207
 Query 204 ILSENNYG-QNFTAASNLPV---LIPVTLPLDL--IQSPSDGRK--HRIGLPVI----- 249
 I+S NN NF + +P+ LIP+ P L + P + +PVI
 Sbjct 208 IISANNRSLANFKPENLVPLASLLIPLNREPALGSLAKPREPNSPFRESSIPVINPHKKK 267
 Query 250 -----IGISLGCTLLVV-----VSAILLVCCCLMKMSLNR-----SASSAETAD 289
 IG+ + T +VV V+A L+V + K ++L++ S S T++
 Sbjct 268 SKMMWIGVYIAVTGVVVGATIAIVAFLIVQLKKKKKQNLKSGDPELQQLSLSVRTTSE 327
 Query 290 KLLS--GVSGYVSKPTM-----YETGAILEATMNLSEQCKIGESVYKANIEG 334
 K+S G + + Y + +AT + S I SVY + G
 Sbjct 328 KKVSEFGSQDLDNQIIDTTPRNRKVLVENYTVEELRKATEDFSSSLIDGSVYVYGRNG 387
 Query 335 KVLAVKREKEDVTEELKILQKVN----HGNIIVKLMGVSSDNDGNCFFVVEYAENGSL 390
 K LA+KR K + ++ N H N+++L+G + F+V+EYA+NGSL++W
 Sbjct 388 KNLAIKRTKSETISKIDFSHFQNATHHHPIIIRLLGTCLSEGSDFSFLVFYAKNGSLKDW 447
 Query 391 L-----FAKSCSETSNRSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSS 441
 L F SC LTW QR+ I +DV++ LQYMH P VHR++ S
 Sbjct 448 LHGGGLAMKNQFIASC-----YCFLTWNQRLKICLDVAVALQYMHIMNPSYVHRNVKSR 501
 Query 442 NILDSNFKAKIANFSMARTF-----TNP-----MMSKIDVF 473
 NI LD F AKI NF MAR TNP + ID+F
 Sbjct 502 NIFLDEEFNAKINFGMARCIEGDTQNTTEIHSNTPSSWSGLYLAPEYIHQGVISPCIDIF 561
 Query 474 AFGVVLIELLTGKKAMTTKEN-GEVVMWLWKDIWKIFDQENREERLRKWMDFKLDNYYPI 532
 AFGVVL+E+L+G++ +T +N GE L + K EN E LR+WMD L Y
 Sbjct 562 AFGVVLLEVLSGKRPIRTPDNKGEESNLLSEKMSILSSENAGE-LREWMDNALGENYSF 620
 Query 533 DYALSLASLAVNCTADKSLSRPTIAEIVLSLSLLTQPS 570
 D A++LA+LA +C ++ RP E+V LS L + S
 Sbjct 621 DTAVTLANLARSCEVEEPLRPNAGELVEKLSRLVEES 658

>ref|NP_566689.2|  CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/ receptor signaling
 protein/ transmembrane receptor protein kinase [Arabidopsis
 thaliana]
 dbj|BAF92788.1|  chitin elicitor receptor kinase 1 [Arabidopsis thaliana]
 Length=617

GENE ID: 821717 CERK1 | CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/
 receptor signaling protein/ transmembrane receptor protein kinase
 [Arabidopsis thaliana] (10 or fewer PubMed links)

Score = 229 bits (583), Expect = 1e-57, Method: Compositional matrix adjust.
 Identities = 165/543 (30%), Positives = 273/543 (50%), Gaps = 77/543 (14%)


Query 81 SNLQHEEDKILIPGQVLLIPVTCGCT-GNRSFANISYEINQGDSFYFVATTLYQNLTNWHA 139
 SN++ ++D++ G +L+P C C G+ N SY+ Q D++ VA + Y NLT +
 Sbjct 71 SNIK-DKDRIQMGSRLVVPFPCECQPGDFLGHNFYSYVRQEDTYERVAISNYANLTTMES 129
 Query 140 VMDLNPGLSQFTPLPIGIQVVIPLFCCKPSKNQLDRGIKYLITHVWQPNNDNVSFVSNKLG 199
 + NP +P+ + + + C C ++ + + +T+ +P D++S ++ G
 Sbjct 130 LQARNP-FPATNPLSATLNVLVNCSGDES-VSKDFGLFVITYPLRPEDLSLSIARSSGV 187
 Query 200 SPQDILSENNGYQNFTAASNL---PVLIPVTLPLDLIQSPSDGRKHKRIGLPVIGISLGC 256
 S DIL N G NF + + + P P P S DG +G VI GI +G
 Sbjct 188 S-ADILQRYNPGVNFNSGNGIVYVPGRDPNGAFPPFKSSKQDG----VGAGVIAGIVIG 242
 Query 257 TLLVVVSAILLVCCCLMKMSLNRSASSA-----ETADKLLSGVSG----- 297
 + +++ + +V K KS S SS+ ++ L SG G
 Sbjct 243 IVALLL-ILFIVYYAYRKNKSKGDSFSSSIPLSTKADHASSTSLQSGGLGAGVSPGIAA 301
 Query 298 -YVSKPTMYETGAILEATMNLSEQCKIGE----SVYKANIEGKVLAVKRFKEDVTE---- 348
 V K + + +AT N + KIG+ +VY A + G+ A+K+ + ++
 Sbjct 302 ISVDKSEVFESELEAKATDNFNLSFKIGQGGFGAVYYAELRGEKAATKKMDMEASKQFLA 361
 Query 349 ELKILQKVNHGNIIVKLMGVSSDNDGNCFFVVEYAENGSL 408
 ELK+L +V+H NLV+L+G + G+ F+VVEY ENG+L + L + R L W
 Sbjct 362 ELKVLTRVHVHVNLRLLIGYCE--GSLFLVVEYVENGNLGQHLHG-----SGREPLPW 412
 Query 409 CQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILDSNFKAKIANFSMARTF----- 460
 +R+ IA+D + GL+Y+HEH P VHRDI S+NIL+D F+AK+A+F + +
 Sbjct 413 TKRVQIALDSARGLEYTHEHTVPVYVHRDIKSANILIDQKFRKAVDFGLTKL TEVGGSA 472
 Query 461 -----TFTNPMMSKIDVFAFGVVLIELLTGKKAMTTKENGVEVVMWLWKDIWK 506
 T + +K+DV+AFGVVL EL++ + A+ E V ++ +

```

Sbjct 473 TRGAMGTFGYMAPETVYGEVSAKVDVYAFGVVLYELISAKGAVVKMT--EAVGEFRGLVG 530
Query 507 IFDQ---EENREERLRKWMDPKLDNYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSL 563
      +F++ E ++EE LRK +DP+L + YP D +A L CT + + RP++ IV++L
Sbjct 531 VFEESEFKETDKEEALRKIIDPRLGDSYPFDSVYKMAELGKACTQENALQLRFSMRYIVVAL 590
Query 564 SLL 566
      S L
Sbjct 591 STL 593

```

>ref|XP_002300098.1|  predicted protein [Populus trichocarpa]

gb|EEE84903.1|  predicted protein [Populus trichocarpa]
Length=680


GENE ID: 7467712 POPTRDRAFT_641782 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score = 224 bits (572), Expect = 2e-56, Method: Compositional matrix adjust.
Identities = 192/629 (30%), Positives = 296/629 (47%), Gaps = 87/629 (13%)

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Query 25 IEAQSQQTNGTNFSCPSNS--PPSCETYVYTIISQSPNFLSLTSVSNIFDTSPLSIARASN 83
      + Q+ + + C SN C+T+ + S F SL+++S IA +
Sbjct 32 LSCQTTSFSDASGTHCNSNGLQDQCKTFAI--LHTSSYFSSLSNLSFYGLDRFVIAATNGF 90
Query 84 QHEEDKLIPGQVLLIPVTCGCTGNRSFANISYEINQGDSEFYFVATTLYQNLTNWHAVMDL 143
      + L Q LLIP+ C C G A ++ +G+SFY ++ +L + LT A+ +
Sbjct 91 SANTEFLPKQPLLIPIIDCKCNGGFFQALVTKTTIKGESFYSISKSL--EGLTTCKAIREK 149
Query 144 NPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRGIKYLITHVWQPNDNVSVFVSNKLGASPD 203
      NPG+S L +Q+ +PL C CPS ++ + L+++ D +S ++ K +P+
Sbjct 150 NPGISPENLNGKVLQVPLRCACPSSTEVIATRLLLSYPVSAAGDTISNLAIKENTTPEA 209
Query 204 ILSENNYG-QNFTAASNLPV---LIPVTLPLPD--IQSPSDGRKH---RIGLPVI----- 249
      I S NN F S +P+ LIP+ P L + P++ H LPVI
Sbjct 210 ITSANNRSLTTFKPTSLVPLTSLIPLGCKPTLGLAKPNEPNLHIPASSLPVINPHKKR 269
Query 250 -----IGISLGCTLLVV-----VSAILLVCCCLMKSLNRSA-----SSAETADK 290
      IG+ + T VV ++A LV K + L++ A S T+DK
Sbjct 270 SKMWRIGVYIAVTGAVGVGSIAIAAFLVIQLKKKKQVLSKEADTELQQLSLSVRTTSDK 329
Query 291 LLS-----GVSGYVSKPTMYETGAILE---ATMNLSEQCKIGESVYKANIEGKVL 337
      +S ++ ET + E AT + + +I SVY + GK L
Sbjct 330 KVSFDDSQNHFDQSITDTPGKVFVETTYTVEELKRATEDFNSSNQIEGVSYPHGRNLGNL 389
Query 338 AVKRFKEDVTE--ELKILQKV--NHGNLVKLMGVSSDNDGNCVFVVEYAENGSLLEEWL-- 391
      A +R + + EL + Q +H N+++++G + F+V+EYA+NGSL++WL
Sbjct 390 AIKRVRQETISKVELGLFQDATHHPNIIRVVGTCLESGPDSFLVFEYAKNGSLKDWLHG 449
Query 392 -FAKSCSETSNSRSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILLDSNFK 450
      A ++ LTW QR+ I +DV++ LQYMH +P VHR+I S NI LD F
Sbjct 450 GLAMKNQFIASCYCFLTWNQRLKICLDVAVALQYMHMHMHESVHRNIKSRNIFLDEEFN 509
Query 451 AKIANFSMARTF-----TNP-----MMSKIDVFAFGVVLIELL 483
      AKI NF MA TNP + S D+F+FGVVL+E+L
Sbjct 510 AKIGNFMAGCVEDDTKEPDFNSTNPASWSLGYLAPEAHQGVVSSSDTIFSGFVVLMEVL 569
Query 484 TGRKAMTT-KENGE-VVMLWKDIWKIFDQEEENREERLRKWMDPKLDNYYPIDYALSLASL 541
      +G+ +T +NGE + L K I I EN +E LR+W+D + Y D A +LA++
Sbjct 570 SGQTPITRPNDNGEGSIWLSKKIKSIL--LSENADE--LREWIDSAMGENYSFDEAATLANI 627
Query 542 AVNCTADKSLSRPTIAEIVLSLSLLTQPS 570
      A CT + RPT EIV L L +S
Sbjct 628 ARACTEEDPSLRPTSGEIVEKLLRLVEES 656

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>ref|XP_002263070.1|  PREDICTED: hypothetical protein [Vitis vinifera]
Length=675

GENE ID: 100264694 LOC100264694 | hypothetical protein LOC100264694
[Vitis vinifera] (10 or fewer PubMed links)

Score = 224 bits (571), Expect = 3e-56, Method: Compositional matrix adjust.
Identities = 182/667 (27%), Positives = 303/667 (45%), Gaps = 91/667 (13%)

```

Query 1 MAVFFVSLTLGAQILYVVLMEFTC----IEAQSQQTNGTNFSCPSN-SPSCETYVYTI 55
      MA + L A L++++ T + ++ + + + C N S C T+ +
Sbjct 1 MAALINNFYLRALFLFLLVSVTLGQSLLSCTSSRDASGYCNGNGSQQCCTGTFALLRT 60
Query 56 QSPNFLSLTSVSNIFDTSPLSIARASNQHEEDKLIPGQVLLIPVTCGCTGNRSFANISY 115
      S + SL ++S LTW QR+ I +DV++ LQYMH +P VHR+I S NI LD F
Sbjct 61 NS-YSSSLFNLFSFYLGIDRFLIAEANGFSADTELLPYNLPILLPIECKCKAGFFQAEITK 119
Query 116 EINQGDSEFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIQVVIPLFCKCPSKNQLDRG 175
      +G+SE+ +A +L + LT A+ + NP + + L ++++IPL C CPS ++L +
Sbjct 120 TTIEGESFFGIAESL--EGLTTCKAIRERNPSIQPWGLADKVRLLIPLRCACPSSELIQE 178
Query 176 IKYLITHVWQPNDNVSVFVSNKLGASPDILSENNY-QNFTAASNLPV---LIPVTLPLD 231
      K L++++ +I S NN G S PV LIP+ P
Sbjct 179 TKLLLSYPVSEGDTPVSLAFKFNNTTSEAIISANNRSGATLRLGSLAPVSSLLIPLRDKPT 238
Query 232 LIQSPSDGRKHRIGLPV-----IIGISLGCTLLVVVSAILL- 267
      L SP+ R+ +GLP + G+++G ++ + + +
Sbjct 239 L-GSPAKPREPNLGLPATSIPIVINPHKKKTKMWKIGVYIAVSGVAVGASVIAAAVLIH 297
Query 268 -----VCVCCCLMKSLNRSASSAETADKLLSGVSGYVSKPTMYETGAILE 312
      + L +++ + S E + + + + ET +LE
Sbjct 298 WKRKKQNAYKMGDVELLQGLSVRTTSEKKVSEFGSQDPIDQIIDSTPHKIVVETTYTMLE 357
Query 313 ---ATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTE--ELKILQKV--NHGNLVKLM 365
      AT + + + I SV+ + GK LA+K + E + +H N++++L+
Sbjct 358 LRKATEDFNSSNLISVFGHRLNGKNLAIKHTHEPAISKIEFGLHDAIHHHPNIMRLL 417
Query 366 GVSSDNDGNCVFVVEYAENGSLLEEWL---FAKSCSETSNSRSLTWCQRISIAVDVSMGL 422
      G + + +++++EYA+NGSL++WL A ++ LTW QR+ I +DV+M L
Sbjct 418 GTCLENGPDSYLIPEYAKNGSLKDWLHGGLAMKSQFIASCYCFLTWNQRLRICLDVAMAL 477

```

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Query 423 QYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNP----- 465
          QYMH +P VHR+I S NI LD F AKI NF MAR F +
Sbjct 478 QYMHMHMPCYVHRNIKS RNIFLDEEFNAKIGNFGMARCFEDDAEDSQPYSTASWSKGYL 537

Query 466 -----MMSKIDVFAFGVVLIELLTGRKAMTTKEN--GEVVMLWKDIWKIFDQEENR 514
          + +D+FA+GVVL+E+L+G+ +T ++ G V L + I I E
Sbjct 538 APEYLHQGIISPTLDIFAYGVVLEVLSGKTPITRADDKGGGRVWLPEKIKSILGSENTE 597

Query 515 EERLRKWMDPKLDNYYPIDYALSASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATL 574
          E LR WMD L Y D A++LA+LA CT + SRP+ EIV LS L + P
Sbjct 598 E--LRDWMSALGENYSFDAAITLANLARVCTDENPCSRPSAGEIVEKLSRLVEQLPEGE 655

Query 575 ERSLTSS 581
          + S+ S
Sbjct 656 QFSICES 662

```

>emb|CB140054.3| unnamed protein product [Vitis vinifera]
Length=672

Score = 224 bits (570), Expect = 4e-56, Method: Compositional matrix adjust.
Identities = 175/644 (27%), Positives = 300/644 (46%), Gaps = 67/644 (10%)

```

Query 1 MAVFFVSLTLGAQILYVVMFFTC---IEAQSQQTNGTNFSCPSN-SPSCETYVITYIS 55
          MA + L A L+++ T + ++ + + + C N S C T+ +
Sbjct 1 MAALINNFYLRALFLFILVFVSTLQGSLLSCTESSRDASGYCNGNGSQKQCGTFALLRT 60

Query 56 QSPNFLSLTSVSNIFDTSPLSIARASNLQHEEDKLIPGQVLLIPVTCGCTGNRSFANISY 115
          S + SL ++S IA A+ + + L LLIP+ C C A ++
Sbjct 61 NS-YYSSLFNL SFYL GIDRFLIAEANGFSADTELLPYNLPLLIPIECKCKAGFFQAE LTK 119

Query 116 EINQGDSEFYFVATTLYQNLTNWHAVMDLNPGLSQFTLPIGIVVPIPLFCCKPSKNQLDRG 175
          +G+SF+ +A +L + LT A+ + NP + + L +++IPL C CPS ++L +
Sbjct 120 TTIEGESFFGIAESL-EGLTTCKAIRERNPSIQPWGLADKVRLLIPLRCACPSSSELIQE 178

Query 176 IKYLITHVWQPNDNVSFVSNKLGASPDILSENNY-QQNFTAASNLP--VLIPVTLPLDL 232
          K L+++ D V ++ K + + I+S NN G S P + +P T +P +
Sbjct 179 TKLLLSYFVSEGDTPVSLAFKFNTTSEAIISANNRSGATLRLGSLAPPNLGLPATSIPIVI 238

Query 233 IQSPSDGRKHRIGLPVII-GISLGCTLLVVVSAILL-----VCVCCCLKM 275
          + +IG+ + + G+++G ++ + + +++ + L +
Sbjct 239 NPHKKKTKMKWIGYIIAVSGVAVGASVAIAAAVLVIHWKRKKQNAYKMGDVELQQLGLSV 298

Query 276 KSLNRSASSAETADKLLSGVSGYVSKPTMYETGAILE---ATMNLSEQCKIGESVYKANI 332
          ++ + S E + + + + ET +LE AT + + I SV+ +
Sbjct 299 RTTSEKKVSEFGSQDPIDQIIDSTPHKIVVETTYTMLELRKATEDFNSSNLIEGVSFHGRL 358

Query 333 EGKVLAVKRFKEDVTE--ELKILQKV--NHGNLVKLMGVSSDNDGNCFFVVEYAENGSL 388
          GK LA+K + E + +H N+++L+G + + +++EYA+NGSL+
Sbjct 359 NGKNLAIKHHTPEAISKIEFGLFHDAIHHPNIMRLLGTCLNEGPD SYLIFEYAKNGSLK 418

Query 389 EWL---FAKSCSETSNRSTSLTWCQRISIAVDVSMGLQYMHEHAYPRIVHRDITSSNILL 445
          +WL A ++ LTW QR+ I +DV+M LQYMH +P VHR+I S NI L
Sbjct 419 DWLHGGLAMKSQFIASCYCFLTWNQRLRICLDVAMALQYMHMHMPCYVHRNIKS RNIFL 478

Query 446 DSNFKAKIANFSMARTFTNP-----MMSKIDVFAFGVVL 479
          D F AKI NF MAR F + + +D+FA+GVVL
Sbjct 479 DEEFNAKIGNFGMARCFEDDAEDSQPYSTASWSKGYLAPEYLHQGIISPTLDIFAYGVVL 538

Query 480 IELLTGRKAMTTKEN--GEVVMLWKDIWKIFDQEENREERLRKWMDFKLDNYYPIDYALS 537
          +E+L+G+ +T ++ G V L + I I E E LR WMD L Y D A++
Sbjct 539 LEVLSGKTPITRADDKGGGRVWLPEKIKSILGSENTEE--LRDWMSALGENYSFDAAIT 596

Query 538 LASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATLERSLTSS 581
          LA+LA CT + SRP+ EIV LS L + P + S+ S
Sbjct 597 LANLARVCTDENPCSRPSAGEIVEKLSRLVEQLPEGEQFSICES 640

```

Select All Get selected sequences Distance tree of results Multiple alignment

APPENDIX B

BLAST**Basic Local Alignment Search Tool**

•

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download!](#)**SEQID48 (598 letters)**Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
Description

SEQID48

Molecule type

amino acid

Query Length

598

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

ProgramBLASTP 2.2.24+ [Citation](#)**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#) [Multiple alignment](#)
[Search Parameters](#)**Search parameter name Search parameter value**

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Filter string	F
Genetic Code	1
Window Size	40
Threshold	11
Composition-based stats	2

Database

Database parameter name Database parameter value

Posted date	Sep 26, 2010 5:43 PM
Number of letters	4,071,357,309
Number of sequences	11,921,515
Entrez query	none

Karlin-Altschul statistics

Params Ungapped Gapped

Lambda	0.318422	0.267
K	0.132723	0.041
H	0.387288	0.14

Results Statistics

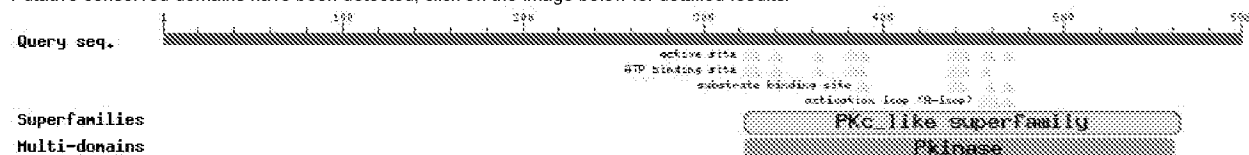
Results Statistics parameter name Results Statistics parameter value

Length adjustment	144
Effective length of query	454
Effective length of database	2354659149
Effective search space	1069015253646
Effective search space used	1069015253646

Graphic Summary

Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.



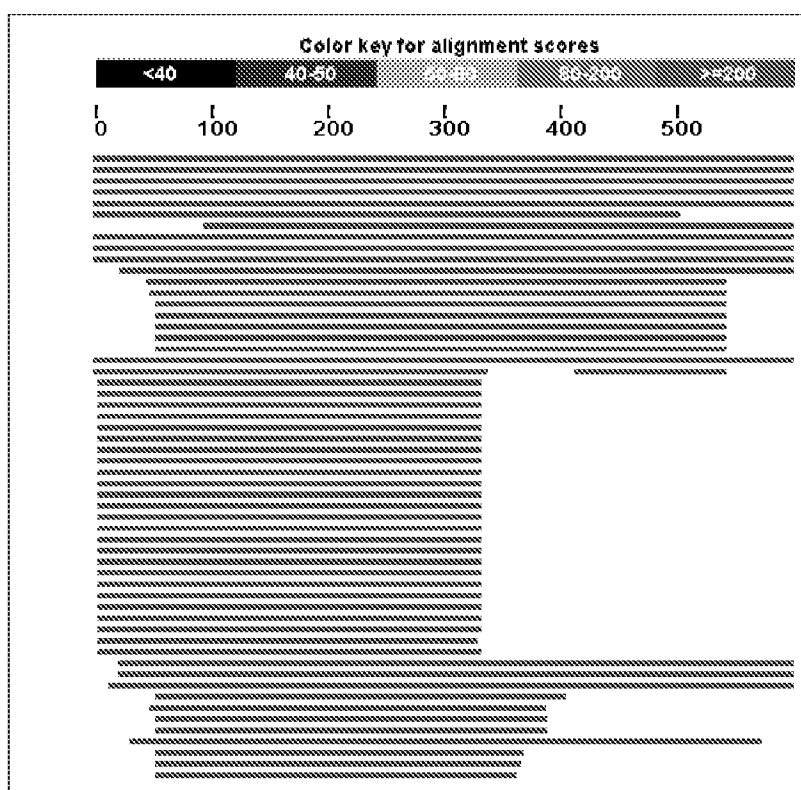
Superfamilies

Multi-domains

Distribution of 102 Blast Hits on the Query Sequence











[?]



















An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Descriptions

Legend for links to other resources:  UniGene  GEO  Gene  Structure  Map Viewer  PubChem BioAssay
Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Links
ABG89809.1	NFR5a [Glycine max] >gb ADJ19105.1 Nod-factor receptor 5A [Glycine max] >gb ADJ19108.1 Nod-factor receptor 5A [Glycine max]	1235	1235	100%	0.0	
ADJ19105.1	Nod-factor receptor 5A [Glycine max]	1235	1233	100%	0.0	
ADJ19107.1	Nod-factor receptor 5A [Glycine max]	1231	1231	100%	0.0	
ADJ19112.1	Nod-factor receptor 5B [Glycine max]	1106	1106	100%	0.0	
ADJ19111.1	Nod-factor receptor 5B [Glycine max]	1103	1103	100%	0.0	
ADJ19110.1	truncated Nod-factor receptor 5A [Glycine max]	1037	1037	83%	0.0	
ABG89813.1	NFR5b [Glycine max]	957	957	84%	0.0	
CAE82593.1	SYM10 protein [Pisum sativum] >emb CAE02594.1 SYM10 protein [Pisum sativum]	899	899	100%	0.0	
CAE82595.1	SYM10 protein [Pisum sativum] >emb CAE02596.1 SYM10 protein [Pisum sativum] >gb ADB45277.1 Nod factor recognition protein [Pisum sativum]	895	895	100%	0.0	
CAE82597.1	Nod-factor receptor 5 [Lotus japonicus] >emb CAE02598.1 Nod-factor receptor 5 [Lotus japonicus]	875	875	100%	0.0	
ABF50224.1	Nod factor perception protein [Medicago truncatula]	864	864	96%	0.0	
CAO02935.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	761	761	82%	0.0	
CAO02938.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	754	754	82%	0.0	
CAO02933.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02934.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02935.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02938.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02939.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02952.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02955.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02957.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02959.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02967.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02971.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02972.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02973.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	747	747	81%	0.0	
CAO02951.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	745	745	81%	0.0	
CAO02949.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	745	745	81%	0.0	
CAO02944.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02970.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	744	744	81%	0.0	
CAO02965.1	LysM-domain containing receptor-like kinase [Medicago truncatula]	741	741	81%	0.0	
BAI79275.1	LysM type receptor kinase [Lotus japonicus] >dbj BAI79285.1 LysM type receptor kinase [Lotus japonicus]	704	704	100%	0.0	
ADJ19109.1	truncated Nod-factor receptor 5A [Glycine max]	695	695	56%	0.0	
BAG85143.1	Nod factor receptor protein [Glycine soja] >dbj BAG85149.1 Nod factor receptor protein [Glycine soja] >dbj BAG85156.1 Nod factor receptor protein [Glycine soja] >dbj BAG85159.1 Nod factor receptor protein [Glycine max] >dbj BAG85160.1 Nod factor receptor protein [Glycine max] >dbj BAG85161.1 Nod factor receptor protein [Glycine max] >dbj BAG85162.1 Nod factor receptor protein [Glycine max] >dbj BAG85165.1 Nod factor receptor protein [Glycine max] >dbj BAG85168.1 Nod factor receptor protein [Glycine max] >dbj BAG85171.1 Nod factor receptor protein [Glycine max] >dbj BAG85174.1 Nod factor receptor protein [Glycine max] >dbj BAG85177.1 Nod factor receptor protein [Glycine max] >dbj BAG85179.1 Nod factor receptor protein [Glycine max] >dbj BAG85180.1 Nod factor receptor protein [Glycine max]	675	675	54%	0.0	
BAG85148.1	Nod factor receptor protein [Glycine soja]	674	674	54%	0.0	
BAG85151.1	Nod factor receptor protein [Glycine soja]	673	673	54%	0.0	
BAG85178.1	Nod factor receptor protein [Glycine max]	673	673	54%	0.0	
BAG85187.1	Nod factor receptor protein [Glycine max]	673	673	54%	0.0	
BAG85164.1	Nod factor receptor protein [Glycine max]	673	673	54%	0.0	
BAG85179.1	Nod factor receptor protein [Glycine max]	672	672	54%	0.0	
BAG85166.1	Nod factor receptor protein [Glycine soja]	672	672	54%	0.0	
BAG85158.1	Nod factor receptor protein [Glycine max]	672	672	54%	0.0	
BAG85144.1	Nod factor receptor protein [Glycine soja] >dbj BAG85145.1 Nod factor receptor protein [Glycine soja]	672	672	54%	0.0	
BAG85142.1	Nod factor receptor protein [Glycine soja]	672	672	54%	0.0	
BAG85152.1	Nod factor receptor protein [Glycine soja]	672	672	54%	0.0	
BAG85175.1	Nod factor receptor protein [Glycine max]	672	672	54%	0.0	
BAG85172.1	Nod factor receptor protein [Glycine max]	671	671	54%	0.0	
BAG85157.1	Nod factor receptor protein [Glycine soja]	671	671	54%	0.0	
BAG85159.1	Nod factor receptor protein [Glycine soja]	671	671	54%	0.0	

BAQ85176.1	Nod factor receptor protein [Glycine max]	670	670	54%	0.0	
BAQ85153.1	Nod factor receptor protein [Glycine soja]	669	669	54%	0.0	
BAQ85155.1	Nod factor receptor protein [Glycine soja]	669	669	54%	0.0	
BAQ85193.1	Nod factor receptor protein [Glycine max]	669	669	54%	0.0	
BAQ85173.1	Nod factor receptor protein [Glycine max]	669	669	54%	0.0	
BAQ85154.1	Nod factor receptor protein [Glycine soja]	667	667	54%	0.0	
BAQ85168.1	Nod factor receptor protein [Glycine max]	665	665	54%	0.0	
BAQ85168.1	Nod factor receptor protein [Glycine max]	660	660	54%	0.0	
BAQ85147.1	Nod factor receptor protein [Glycine soja]	659	659	54%	0.0	
XP_002289472.1	PREDICTED: hypothetical protein [Vitis vinifera] >emb CBI17584.3 unnamed protein product [Vitis vinifera]	654	654	96%	0.0	
XP_002533280.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF29112.1 serine-threonine protein kinase, plant-type, putative [Ricinus communis]	638	638	96%	0.0	
XP_002310198.1	predicted protein [Populus trichocarpa] >gb EEE90648.1 predicted protein [Populus trichocarpa]	614	614	97%	1e-173	
CAQ02236.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	499	499	58%	4e-139	
CAQ02248.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	484	484	56%	2e-134	
CAQ02242.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	481	481	56%	1e-133	
CAQ02299.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	477	477	55%	2e-132	
XP_002468236.1	hypothetical protein SORBDRAFT_01g042230 [Sorghum bicolor] >gb EER95234.1 hypothetical protein SORBDRAFT_01g042230 [Sorghum bicolor]	441	441	90%	2e-121	
CAQ02293.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	436	436	52%	6e-120	
CAQ02264.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula] >emb CAO02968.1 LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	433	433	52%	4e-119	
CAQ02244.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	427	427	51%	2e-117	
AAM19130.1	Putative protein kinase [Oryza sativa Japonica Group] >gb ABF94815.1 Protein kinase domain containing protein [Oryza sativa (japonica cultivar-group)] >gb EAZ26175.1 hypothetical protein OsJ_10042 [Oryza sativa Japonica Group]	426	426	93%	3e-117	
EAY38155.1	hypothetical protein OsJ_10648 [Oryza sativa Indica Group]	426	426	93%	6e-117	
CAQ02248.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	422	422	51%	6e-116	
CAQ02262.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	418	418	51%	9e-115	
XP_002517929.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF45192.1 serine-threonine protein kinase, plant-type, putative [Ricinus communis]	366	366	86%	5e-99	
XP_002238070.1	PREDICTED: hypothetical protein [Vitis vinifera]	355	355	89%	8e-96	
AA100791.1	SYM10-like protein [Galega orientalis]	351	351	40%	2e-94	
CBI26359.3	unnamed protein product [Vitis vinifera]	345	345	89%	1e-92	
ABR17883.1	unknown [Picea sitchensis]	343	343	76%	3e-92	
CAN89762.1	hypothetical protein [Vitis vinifera]	338	338	89%	1e-90	
XP_002311652.1	predicted protein [Populus trichocarpa] >gb EEE89020.1 predicted protein [Populus trichocarpa]	324	324	76%	2e-86	
CAQ02299.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	313	313	40%	6e-83	
EAY87982.1	hypothetical protein OsJ_08480 [Oryza sativa Indica Group]	313	313	88%	6e-83	
XP_001767824.1	predicted protein [Phycomitrella patens subsp. patens] >gb EDQ67338.1 predicted protein [Phycomitrella patens subsp. patens]	302	302	91%	8e-80	
BAI79275.1	LysM type receptor kinase [Lotus japonicus]	297	297	92%	2e-78	
XP_002326901.1	predicted protein [Populus trichocarpa] >gb EEE73651.1 predicted protein [Populus trichocarpa]	292	292	86%	8e-77	
XP_001763589.1	predicted protein [Phycomitrella patens subsp. patens] >gb EDQ51621.1 predicted protein [Phycomitrella patens subsp. patens]	291	291	90%	2e-76	
BAI79277.1	LysM type receptor kinase [Lotus japonicus] >dbj BAI79287.1 LysM type receptor kinase [Lotus japonicus]	286	286	87%	4e-75	
XP_002519756.1	kinase, putative [Ricinus communis] >gb EEF52943.1 kinase, putative [Ricinus communis]	283	283	85%	5e-74	
XP_002522589.1	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis] >gb EEF39869.1 BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]	280	280	86%	3e-73	
XP_002980895.1	hypothetical protein SELMODRAFT_11326 [Selaginella moellendorffii] >gb EFJ08078.1 hypothetical protein SELMODRAFT_11326 [Selaginella moellendorffii]	280	280	89%	3e-73	
XP_002277331.1	PREDICTED: hypothetical protein [Vitis vinifera]	280	280	91%	4e-73	
XP_002974495.1	hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii] >gb EFJ24716.1 hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii]	279	279	89%	7e-73	
Q8H17583.3	unnamed protein product [Vitis vinifera]	277	551	88%	3e-72	
XP_002519333.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF52520.1 serine-threonine protein kinase, plant-type, putative [Ricinus communis]	276	276	86%	5e-72	
BAI79278.1	LysM type receptor kinase [Lotus japonicus]	276	276	91%	7e-72	
BAI79286.1	LysM type receptor kinase [Lotus japonicus]	276	276	91%	8e-72	
A6Q88912.1	LYK4 [Glycine max]	270	270	96%	5e-70	
CBI46796.3	unnamed protein product [Vitis vinifera]	269	347	82%	1e-69	
XP_002269442.1	PREDICTED: hypothetical protein [Vitis vinifera]	268	268	88%	1e-69	
XP_002533279.1	serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gb EEF29111.1	265	265	90%	2e-68	

	serine-threonine protein kinase, plant-type, putative [Ricinus communis]					
XP_002533278.1	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis] >gb EEF29110.1 BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]	265	265	89%	2e-68	
XP_002255408.1	PREDICTED: hypothetical protein [Vitis vinifera]	263	263	86%	4e-68	
XP_002327712.1	predicted protein [Populus trichocarpa] >gb EEE75190.1 predicted protein [Populus trichocarpa]	258	258	86%	2e-66	
XP_002319777.1	predicted protein [Populus trichocarpa] >gb EEE91227.1 predicted protein [Populus trichocarpa]	254	254	86%	2e-65	
XP_002231889.1	PREDICTED: hypothetical protein [Vitis vinifera]	253	253	86%	4e-65	
XP_002509549.1	ATP binding protein, putative [Ricinus communis] >gb EEF50927.1 ATP binding protein, putative [Ricinus communis]	253	253	88%	4e-65	
NP_001958119.1	Os06g0625200 [Oryza sativa Japonica Group] >dbj BAD35689.1 receptor protein kinase-like [Oryza sativa Japonica Group] >dbj BAD37734.1 receptor protein kinase-like [Oryza sativa Japonica Group] >dbj BAF20024.1 Os06g0625200 [Oryza sativa Japonica Group] >gb EAZ37689.1 hypothetical protein OsJ_22029 [Oryza sativa Japonica Group]	251	251	86%	3e-64	
XP_002307839.1	predicted protein [Populus trichocarpa] >gb EEE94826.1 predicted protein [Populus trichocarpa]	248	248	86%	2e-63	
CAQ92861.1	LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]	240	240	21%	4e-61	
XP_002350098.1	predicted protein [Populus trichocarpa] >gb EEE84903.1 predicted protein [Populus trichocarpa]	238	238	93%	2e-60	
NP_558898.2	CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/ receptor signaling protein/ transmembrane receptor protein kinase [Arabidopsis thaliana] >dbj BAF92788.1 chitin elicitor receptor kinase 1 [Arabidopsis thaliana]	236	236	80%	8e-60	
CEM4094.3	unnamed protein product [Vitis vinifera]	234	234	95%	2e-59	
XP_002263079.1	PREDICTED: hypothetical protein [Vitis vinifera]	233	233	95%	4e-59	

Alignments

Select All Get selected sequences Distance tree of results Multiple alignment

>gb|ABQ59609.1| NFR5a [Glycine max]
 gb|ADJ19105.1| Nod-factor receptor 5A [Glycine max]
 gb|ADJ19108.1| Nod-factor receptor 5A [Glycine max]
 Length=598

Score = 1235 bits (3196), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 598/598 (100%), Positives = 598/598 (100%), Gaps = 0/598 (0%)

Query	1	MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPSCETYVVTYIAQSPN	60
Sbjct	1	MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPSCETYVVTYIAQSPN	60
Query	61	FLSLTNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQ	120
Sbjct	61	FLSLTNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQ	120
Query	121	GDSFYFVATTSYENLTNWRVMDLNPVLSNKLPIGIVVFPLFCCKPSKNQLDKEIKYL	180
Sbjct	121	GDSFYFVATTSYENLTNWRVMDLNPVLSNKLPIGIVVFPLFCCKPSKNQLDKEIKYL	180
Query	181	ITYVWKPGDNVLSVSKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDG	240
Sbjct	181	ITYVWKPGDNVLSVSKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDG	240
Query	241	RKGGIRLPVITIGISLGCTLLVVLAVLLVYVYCLMKTLNRSASSAETADKLLSGVSGYV	300
Sbjct	241	RKGGIRLPVITIGISLGCTLLVVLAVLLVYVYCLMKTLNRSASSAETADKLLSGVSGYV	300
Query	301	SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVRKFKEDVTEELKILQKVNHG	360
Sbjct	301	SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVRKFKEDVTEELKILQKVNHG	360
Query	361	NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSSKSCSDTSNSRASLTWCQRISMAVDVA	420
Sbjct	361	NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSSKSCSDTSNSRASLTWCQRISMAVDVA	420
Query	421	MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMPKIDVFAFGVVL	480
Sbjct	421	MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMPKIDVFAFGVVL	480
Query	481	IELLTGRKAMTTKENGVEVVLWKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYALSLA	540
Sbjct	481	IELLTGRKAMTTKENGVEVVLWKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYALSLA	540
Query	541	SLAVNCTADKSLSRPTIAEIVLSLSLTQPSPATLERSLTSSGLDVEATQIVTSIAAR	598
Sbjct	541	SLAVNCTADKSLSRPTIAEIVLSLSLTQPSPATLERSLTSSGLDVEATQIVTSIAAR	598


>gb|ADJ19106.1| Nod-factor receptor 5A [Glycine max]
 Length=598

GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
 (10 or fewer PubMed links)

Score = 1233 bits (3189), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 597/598 (99%), Positives = 598/598 (100%), Gaps = 0/598 (0%)

Query	1	MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPSCETYVVTYIAQSPN	60
		MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPSCETYVVTYIAQSPN	


Sbjct	1	MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPSPSCETYVVTYIAQSPN	60
Query	61	FLSLTNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQ	120
		FLSLTNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQ	
Sbjct	61	FLSLTNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQ	120
Query	121	GDSFYFVATTSSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCCKCPSKNQLDKEIKYL	180
		GDSFYFVATTSSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCCKCPSKNQLDKEIKYL	
Sbjct	121	GDSFYFVATTSSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCCKCPSKNQLDKEIKYL	180
Query	181	ITYVWKPGDNVSLVSDKFGASPEDIMSENNGQNFATAANNLPVLIPVTRLPVLARSPSDG	240
		ITYVWKPGDNVSLVSDKFGASPEDIMSENNGQNFATAANNLPVLIPVTRLPVLARSPSDG	
Sbjct	181	ITYVWKPGDNVSLVSDKFGASPEDIMSENNGQNFATAANNLPVLIPVTRLPVLARSPSDG	240
Query	241	RKGGIRLPVLIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSSASSAETADKLLSGVSGYV	300
		RKGGIRLPVLIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSSASSAETADKLLSGVSGYV	
Sbjct	241	RKGGIRLPVLIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSSASSAETADKLLSGVSGYV	300
Query	301	SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHG	360
		SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHG	
Sbjct	301	SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHG	360
Query	361	NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSSKSCSDTSNSRASLTWCQRISMAVDVA	420
		NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSSKSCSDTSNSRASLTWCQRISMAVDVA	
Sbjct	361	NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSSKSCSDTSNSRASLTWCQRISMAVDVA	420
Query	421	MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL	480
		MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL	
Sbjct	421	MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL	480
Query	481	IELLTGKRAMTTKENGEEVVMWLKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYALSLA	540
		IELLTGKRA+TTKENGEEVVMWLKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYALSLA	
Sbjct	481	IELLTGKRAVTTKENGEEVVMWLKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYALSLA	540
Query	541	SLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATLERSLTSSGLDVEATQIVTSIAAR	598
		SLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATLERSLTSSGLDVEATQIVTSIAAR	
Sbjct	541	SLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATLERSLTSSGLDVEATQIVTSIAAR	598

>gb|ADJ19107.1|  Nod-factor receptor 5A [Glycine max]
Length=598

GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
(10 or fewer PubMed links)

Score = 1231 bits (3184), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 596/598 (99%), Positives = 598/598 (100%), Gaps = 0/598 (0%)

Query	1	MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPSPSCETYVVTYIAQSPN	60
		MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPSPSCETYVVTYIAQSPN	
Sbjct	1	MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPSPSCETYVVTYIAQSPN	60
Query	61	FLSLTNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQ	120
		FLSLTNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQ	
Sbjct	61	FLSLTNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQ	120
Query	121	GDSFYFVATTSSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCCKCPSKNQLDKEIKYL	180
		GDSFYFVATTSSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCCKCPSKNQLDKEIKYL	
Sbjct	121	GDSFYFVATTSSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCCKCPSKNQLDKEIKYL	180
Query	181	ITYVWKPGDNVSLVSDKFGASPEDIMSENNGQNFATAANNLPVLIPVTRLPVLARSPSDG	240
		ITYVWKPGDNVSLVSDKFGASPEDIMSENNGQNFATAANNLPVLIPVTRLPVLARSPSDG	
Sbjct	181	ITYVWKPGDNVSLVSDKFGASPEDIMSENNGQNFATAANNLPVLIPVTRLPVLARSPSDG	240
Query	241	RKGGIRLPVLIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSSASSAETADKLLSGVSGYV	300
		RKGGIRLPVLIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSSASSAETADKLLSGVSGYV	
Sbjct	241	RKGGIRLPVLIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSSASSAETADKLLSGVSGYV	300
Query	301	SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHG	360
		SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFK+DVTEELKILQKVNHG	
Sbjct	301	SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKDVTEELKILQKVNHG	360
Query	361	NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSSKSCSDTSNSRASLTWCQRISMAVDVA	420
		NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSSKSCSDTSNSRASLTWCQRISMAVDVA	
Sbjct	361	NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSSKSCSDTSNSRASLTWCQRISMAVDVA	420
Query	421	MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL	480
		MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL	
Sbjct	421	MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL	480
Query	481	IELLTGKRAMTTKENGEEVVMWLKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYALSLA	540
		IELLTGKRA+TTKENGEEVVMWLKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYALSLA	
Sbjct	481	IELLTGKRAVTTKENGEEVVMWLKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYALSLA	540
Query	541	SLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATLERSLTSSGLDVEATQIVTSIAAR	598
		SLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATLERSLTSSGLDVEATQIVTSIAAR	
Sbjct	541	SLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATLERSLTSSGLDVEATQIVTSIAAR	598

>gb|ADJ19112.1|  Nod-factor receptor 5B [Glycine max]
Length=599

GENE ID: 100498857 NFR5b | Nod-factor receptor 5B [Glycine max]
(10 or fewer PubMed links)

Score = 1106 bits (2861), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 563/599 (93%), Positives = 578/599 (96%), Gaps = 1/599 (0%)

Query	1	MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPSPSC-ETYVVTYIAQSP	59
		MAVFF FLPL SQILCLV+MLE TNIVAQSQQ N TNFSCPSDSPP ETYVVTYIAQSP	
Sbjct	1	MAVFFSFLPLRSQILCLVLMFFTNIVAQSQQTNFSCPSDSPSPSCETYVVTYIAQSP	60
Query	60	NFLSLTNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEIN	119
		NFLSLT+ISNIFDTSPLSIARASNLEP DDKL+ DQVLL+PVTCGCTGNRSFANISYEIN	
Sbjct	61	NFLSLTISNIFDTSPLSIARASNLEPEDDKLIADQVLLIPVTCGCTGNRSFANISYEIN	120
Query	120	QGDSFYFVATTSSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCCKCPSKNQLDKEIKY	179

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Sbjct 121 GDSFYFVATTSYENLNTNWR VMDLNP LSPN LPIGIGVVFPLFCKCPSKNQLDK IKY 180
PGDSFYFVATTSYENLNTNWRVMDLNPSPSLPNTLPIGIGVVFPLFCKCPSKNQLDKGIKY

Query 180 LITYVWKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLI PVTRLPVLARSPSD 239
LITYVW+P DNVSLVS+KFGASPEDI+SENNYGQNFATAANNLPVLI PVTRLPVLA+SPSD

Sbjct 181 LITYVWQPSDNVSLVSEKFGASPEDILSENNYGQNFATAANNLPVLI PVTRLPVLAQSPSD 240

Query 240 GRKGGIRLPVIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSSASSAETADKLLSGVSGY 299
RKGGIRLPVIGISLGCTLLV+VLAVLLVYVYCLK+K+LNRSSASSAETADKLLSGVSGY

Sbjct 241 VRKGGIRLPVIGISLGCTLLVVVLAVLLVYVYCLKIKSLNRSSASSAETADKLLSGVSGY 300

Query 300 VSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKQVNH 359
VSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKE+VTEELKILQKQVNH

Sbjct 301 VSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKENVTEELKILQKQVNH 360

Query 360 GNLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFKSCSDTSNSRASLTWCQRISMAVDV 419
GNLVKLMGVSSDNDGNCFFVVEYA+NGSLDEWLF KSCSDTS+SRASLTWCQRIS+AVDV

Sbjct 361 GNLVKLMGVSSDNDGNCFFVVEYAQNGSLDEWLFYKSCSDTSDSRASLTWCQRISIAVDV 420

Query 420 AMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMPMKIDVFAFGVV 479
AMGLQYMHEHAYPRIVHRDI SSNILLDSNFKAKIANFSMARTFTNP MPKIDVFAFGVV


Sbjct 421 AMGLQYMHEHAYPRIVHRDIASSNILLDSNFKAKIANFSMARTFTNPMPKIDVFAFGVV 480

Query 480 LIELLTGRKAMTTKENGVEVMLWKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYALSL 539
LIELLTGRKAMTTKENGVEVMLWKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYALSL

Sbjct 481 LIELLTGRKAMTTKENGVEVMLWKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYALSL 540

Query 540 ASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATLERSLTSSGLDVEATQIVTSIAAR 598
ASLAVNCTADKSLSR TIAEIVLSLSLLTQPSPATLERSLTSSGLDVEATQIVTSIAAR

Sbjct 541 ASLAVNCTADKSLSRSTIAEIVLSLSLLTQPSPATLERSLTSSGLDVEATQIVTSIAAR 599
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>gb|ADJ19111.1|  Nod-factor receptor 5B [Glycine max]
Length=599

GENE ID: 100498857 NFR5b | Nod-factor receptor 5B [Glycine max]
(10 or fewer PubMed links)

Score = 1103 bits (2854), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 562/599 (93%), Positives = 577/599 (96%), Gaps = 1/599 (0%)

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Query 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCPSDSPSPSC-ETYVITYIAQSP 59
MAVFF FLPL SQILCLV+MLF TNIVAQSQQ N TNFCPSDSPSP ETYVITYIAQSP

Sbjct 1 MAVFFSLPLRSQILCLVIMLFSTNIVAQSQQTNETNFCPSDSPSPSCETYVITYIAQSP 60

Query 60 NFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEIN 119
NFLSLT+ISNIFDTSPLSIARASNLEP DDKL+ DQVLL+PVTGCTGNRSFANISYEIN

Sbjct 61 NFLSLTISNIFDTSPLSIARASNLEPEDDKLIADQVLLIPVTCGCTGNRSFANISYEIN 120

Query 120 QGDSFYFVATTSYENLNTNWRVMDLNPVLSPNKLP IGIQVVFPLFCKCPSKNQLDKKEIKY 179
GDSFYFVATTSYENLNTNWR VMDLNP LSPN LPIGIGVVFPLFCKCPSKNQLDK IKY

Sbjct 121 PGDSFYFVATTSYENLNTNWRVMDLNPSPSLPNTLPIGIGVVFPLFCKCPSKNQLDKGIKY 180

Query 180 LITYVWKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLI PVTRLPVLARSPSD 239
LITYVW+P DNVSLVS+KFGASPEDI+SENNYGQNFATAANNLPVLI PVTRLPVLA+SPSD

Sbjct 181 LITYVWQPSDNVSLVSEKFGASPEDILSENNYGQNFATAANNLPVLI PVTRLPVLAQSPSD 240

Query 240 GRKGGIRLPVIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSSASSAETADKLLSGVSGY 299
RKGGIRLPVIGISLGCTLLV+VLAVLLVYVYCLK+K+LNRSSASSAETADKLLSGVSGY

Sbjct 241 VRKGGIRLPVIGISLGCTLLVVVLAVLLVYVYCLKIKSLNRSSASSAETADKLLSGVSGY 300

Query 300 VSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKQVNH 359
VSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKE+VTEELKILQKQVNH

Sbjct 301 VSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKENVTEELKILQKQVNH 360

Query 360 GNLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFKSCSDTSNSRASLTWCQRISMAVDV 419
GNLVKLMGVSSDNDGNCFFVVEYA+NGSLDEWLF KSCSDTS+SRASLTWCQRIS+AVDV

Sbjct 361 GNLVKLMGVSSDNDGNCFFVVEYAQNGSLDEWLFYKSCSDTSDSRASLTWCQRISIAVDV 420

Query 420 AMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMPMKIDVFAFGVV 479
AMGLQYMHEHAYPRIVHRDI SSNILLDSNFKAKIANFSMARTFTNP MPKIDVFAFGVV


Sbjct 421 AMGLQYMHEHAYPRIVHRDIASSNILLDSNFKAKIANFSMARTFTNPMPKIDVFAFGVV 480

Query 480 LIELLTGRKAMTTKENGVEVMLWKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYALSL 539
LIELLTGRKAMTTKENGVEVMLWKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYALSL

Sbjct 481 LIELLTGRKAMTTKENGVEVMLWKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYALSL 540

Query 540 ASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATLERSLTSSGLDVEATQIVTSIAAR 598
ASLAVNCTADKSLSR TIAEIVLSLSLLTQPS PATLERSLTSSGLDVEATQIVTSIAAR

Sbjct 541 ASLAVNCTADKSLSRSTIAEIVLSLSLLTQPS PTLERSLTSSGLDVEATQIVTSIAAR 599
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>gb|ADJ19110.1|  truncated Nod-factor receptor 5A [Glycine max]
Length=501

GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
(10 or fewer PubMed links)

Score = 1037 bits (2682), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 501/501 (100%), Positives = 501/501 (100%), Gaps = 0/501 (0%)

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Query 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCPSDSPSPSCETYVITYIAQSPN 60
MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCPSDSPSPSCETYVITYIAQSPN

Sbjct 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCPSDSPSPSCETYVITYIAQSPN 60

Query 61 FLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQ 120
FLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQ

Sbjct 61 FLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQ 120

Query 121 GDSFYFVATTSYENLNTNWRVMDLNPVLSPNKLP IGIQVVFPLFCKCPSKNQLDKKEIKYL 180
GDSFYFVATTSYENLNTNWRVMDLNPVLSPNKLP IGIQVVFPLFCKCPSKNQLDKKEIKYL

Sbjct 121 GDSFYFVATTSYENLNTNWRVMDLNPVLSPNKLP IGIQVVFPLFCKCPSKNQLDKKEIKYL 180

Query 181 IITYVWKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLI PVTRLPVLARSPSDG 240
IITYVWKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLI PVTRLPVLARSPSDG

Sbjct 181 IITYVWKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLI PVTRLPVLARSPSDG 240
```

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Query   241   RKG GIRLPV IIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYV   300
          RKG GIRLPV IIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYV
Sbjct   241   RKG GIRLPV IIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYV   300

Query   301   SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHG   360
          SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHG
Sbjct   301   SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHG   360

Query   361   NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMAVDVA   420
          NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMAVDVA
Sbjct   361   NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMAVDVA   420

Query   421   MGLQYMH E HAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL   480
          MGLQYMH E HAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL
Sbjct   421   MGLQYMH E HAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVL   480

Query   481   IELLTGRKAMTTKENG EVVVL 501
          IELLTGRKAMTTKENG EVVVL
Sbjct   481   IELLTGRKAMTTKENG EVVVL 501

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>gb|ABQ59613.1| NFR5b [Glycine max]
Length=515

Score = 957 bits (2475), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 478/504 (94%), Positives = 491/504 (97%), Gaps = 0/504 (0%)

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Query   95   QVLLVPVTCGCTGNRSFANISYEINQGDSFYFVATTSYENLTNWRVMDLNPVLSPNKLP   154
          QVLL+PVTTCGCTGNRSFANISYEIN GDSF FVATTSYENLTNWR VMDLNP LSPN LP
Sbjct   12   QVLLIPVTCGCTGNRSFANISYEINPGDSFNFVATTSYENLTNWRVMDLNPVLSPNLTP   71

Query   155  IGIQVVFPLFCCKPSKNQLDKEIKYLITYVWKP GDNVSLVSKDFGASPEDIMSENNYQGN   214
          IGIQVVFPLFCCKPSKNQLDK IKYLITYVW+P DNVSLVS+KFGASPEDI+SENNYQGN
Sbjct   72   IGIQVVFPLFCCKPSKNQLDKGIKYLITYVWQPSDNVSLVSEKFGASPEDILSENNYQGN   131

Query   215  FTAANNLPVLIPVTRLPVLARSPSDGRKG GIRLPV IIGISLGCTLLVLVLAVLLVYVYCL   274
          FTAANNLPVLIPVTRLPVLA+ PSD RKG GIRLPV IIGISLGCTLLV+VLAVLLVYVYCL
Sbjct   132  FTAANNLPVLIPVTRLPVLAQFPSPDVRKG GIRLPV IIGISLGCTLLVVVLAVLLVYVYCL   191

Query   275  KMKTLNRSASSAETADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIE   334
          K+K+LNRSASSAETADKLLSGVSGYVSKPTMYETDAIMEATMNLSE+CKIGESVYKANIE
Sbjct   192  KIKSLNRSASSAETADKLLSGVSGYVSKPTMYETDAIMEATMNLSECKCKIGESVYKANIE   251

Query   335  GKVLAVKRFKEDVTEELKILQKVNHG NLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFS   394
          GKVLAVKRFE+VTEELKILQKVNHG NLVKLMGVSSDNDGNCFFVVEYA+NGSLDEWLF
Sbjct   252  GKVLAVKRFKENVTEELKILQKVNHG NLVKLMGVSSDNDGNCFFVVEYAQNGSLDEWLFY   311

Query   395  KSCSDTSNSRASLTWCQRISMAVDVAMGLQYMH E HAYPRIVHRDITSSNILLDSNFKAKI   454
          KSCSDTS+SRASLTWCQRIS+AVDVAMGLQYMH E HAYPRIVHRDI SSNILLDSNFKAKI
Sbjct   312  KSCSDTSDSRASLTWCQRISIAVDVAMGLQYMH E HAYPRIVHRDIASSNILLDSNFKAKI   371

Query   455  ANFSMARTFTNPMMPKIDVFAFGVVLIELLTGRKAMTTKENG EVVMLWKDIWKIFDQ EEN   514
          ANFSMARTFTNP MPKIDVFAFGVVLIELLTGRKAMTTKENG EVVMLWKDIWKIFDQ EEN
Sbjct   372  ANFSMARTFTNPMPKIDVFAFGVVLIELLTGRKAMTTKENG EVVMLWKDIWKIFDQ EEN   431

Query   515  REERLKKWMDPKLESYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPAT   574
          REERLKKWMDPKLESYYPIDYALSLASLAVNCTADKSLSR TIAEIVLSLSLLTQPSPAT
Sbjct   432  REERLKKWMDPKLESYYPIDYALSLASLAVNCTADKSLSRSTIAEIVLSLSLLTQPSPAT   491

Query   575  LERSLTSSGLDVEATQIVT SIAAR 598
          LERSLTSSGLDVEATQIVT SIAAR
Sbjct   492  LERSLTSSGLDVEATQIVT SIAAR 515

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>emb|CAE02593.1| SYM10 protein [Pisum sativum]
>emb|CAE02594.1| SYM10 protein [Pisum sativum]
Length=594

Score = 899 bits (2322), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 451/600 (75%), Positives = 505/600 (84%), Gaps = 8/600 (1%)

```

Query   1   MAVFFPFLPHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPPCSETYVTVYIAQSPN   60
          MA+FF LP S L L +M F TN I AQ Q + TNFSCP DSPPCSETYVTVY A+SPN
Sbjct   1   MATIFF--LPSSSHALFLALMFFVTNISAQPLQLSGTNFSCFVDSPPPCSETYVTVYFARSPN   58

Query   61  FLSLTNISNIFDTSPLSIARASNLEPMDDKLKVDQVLLVPVTCGCTGNRSFANISYEINQ   120
          FLSLTNIS+IFD SPLSIA+ASN+E D KLV+ QVLL+PVTTCGCT NR FAN +Y I
Sbjct   59  FLSLTNISDIFDMSPLSIARASNIEDEKKLVGEQVLLIPVTCGCTRNRYFANFTYTIKL   118

Query   121  GDSFYFVATTSYENLTNWRVMDLNPVLSPNKLP IGIQVVFPLFCCKPSKNQLDKEIKYL   180
          GD+++ V+TTSY+NLTN+ + + NP LSPN LP I+VV PLFCCKPSKNQL K IK+L
Sbjct   119  GDNYFIIVTTSYQNLNTNYVEMENFNPNLSPNLLPPEIKVVVPLFCCKPSKNQLSKGIKHL   178

Query   181  ITYVWKP GDNVSLVSKDFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPVLARSPSDG   240
          ITYVW+ DNV+ VS KFGAS D+ +ENN QNFTA+ N+P+LIPVT+LPV+ + S+G
Sbjct   179  ITYVWQANDNVTRVSSKFGASQVDMFTENN--QNFTASTNPILIPVTKLPVIDQPSNG   236

Query   241  RKG GIRLPV--IIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGY   299
          RK + P IIGISLGC V+VL + LVYVYCLMKM LNRS S AETADKLLSGVSGY
Sbjct   237  RKNSTQKPAFIIGISLCAFFVVVLTLSLVYVYCLMKMLNRNSTSLAETADKLLSGVSGY   296

Query   300  VSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNH   359
          VSKPTMYE DAIMEATMNLSE CKIGESVYKANI+G+VLAVK+ K+D +EELKILQKVNH
Sbjct   297  VSKPTMYEMDAIMEATMNLSENCKIGESVYKANIDGRVLAVKKIKKDAEELKILQKVNH   356

Query   360  GNLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMAVDV   419
          GNLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFS+S S TSNS SLTW QRI++AVDV
Sbjct   357  GNLVKLMGVSSDNDGNCFLVVEYAENGSLDEWLFS+S S SKTSNSVVSLTWSQRTIVAVDV   415

Query   420  AMGLQYMH E HAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVV   479
          A+GLQYMH E YPRI+HRDIT+SNILLDSNFKAKIANFSMART TN MMPKIDVFAFGVV
Sbjct   416  AVGLQYMH E HTY PRI+HRDITTSNILLDSNFKAKIANFSMARTSTNSMMPKIDVFAFGVV   475

Query   480  LIELLTGRKAMTTKENG EVVMLWKDIWKIFDQ EENREERLKKWMDPKLESYYPIDYALSL   539
          LIELLTG+KA+TT ENG EVV+LWKD WKIFD E NREE L+KWM DPKE++YPID ALSL
Sbjct   476  LIELLTGKKAITTMENG EVVILWKDFWKIFDLEGNREESLRKWM DPKENFYPIDNALS   535

Query   540  ASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPA-TLERSLTSSGLDVEATQIVT SIAAR   598

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Sbjct 536 ASLAVNCTADKSLSRP+IAEIVL LSL L Q S LERSLT SGLDVEAT +VTSI AR 594
ASLAVNCTADKSLSRPSIAEIVLCLSLNQSSEPMLESLT-SGLDVEATHVVTISIVAR

>emb|CAE02595.1| SYM10 protein [Pisum sativum]
emb|CAE02596.1| SYM10 protein [Pisum sativum]
gb|ADB45277.1| Nod factor recognition protein [Pisum sativum]
Length=594

Score = 895 bits (2312), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 449/600 (74%), Positives = 504/600 (84%), Gaps = 8/600 (1%)

Query 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETVVTYIAQSPN 60
MA+FF LP S L L +M F TNI AQ Q + TNFSCP DSPSCETVVTY A+SPN
Sbjct 1 MAIFF--LPSSSHALFLALMFFVTNISAQPLQLSGTNFSCPVDSPPSCETVVTYFARSPN 58

Query 61 FLSLTNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQ 120
FLSLTNIS+IFD SPLSIA+ASN+E D KLV+ QVLL+PVTGCT NR FAN +Y I
Sbjct 59 FLSLTNISDIFDMSPLSIARASNIEDEDKKLVGEQVLLIPVTCGCTRNRYFANFTYTIKL 118

Query 121 GDSFYFVATTSYENLTNWRVMDLNPVLSPNKLPFIGIQVVFPLFCCKPSKNQLDKEIKYL 180
GD+++ V+TTSY+NLTN+ + + NP LSPN LP I+VV PLFCCKPSKNQL K IK+L
Sbjct 119 GDNFYFVSTTSYQNLNTNYVEMENFNPNLSPNLLPPEIKVVVPLFCCKPSKNQLSKGIKHL 178

Query 181 ITYVWKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLPVTRLPVLARSPSDG 240
ITYVW+ DNV+ VS KFGAS D+ +ENN QNFATA+ N+P+LIPVT+LPV+ + S+G
Sbjct 179 ITYVWQANDNVTRVSSKFGASQVDMFTENN--QNFATA+ N+P+LIPVT+LPV+ + S+G 236

Query 241 RKGGRILPVP--IIGISLGLCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGY 299
RK + P IIGISLGC V+VL + LVYVYCLMK LNRS S AETADKLLSGVSGY
Sbjct 237 RKNSTQKPAFIIGISLGCFFVVLVTLVYVYCLMKMLNRSTSLAETADKLLSGVSGY 296



Query 300 VSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVN 359
VSKPTMYE DAIMEATMNLSE CKIGESVYKANI+G+VLAVK+ K+D +EELKILQKVN
Sbjct 297 VSKPTMYEMDAIMEATMNLSENCKIGESVYKANIDGRVLAVKKIKKDAEELKILQKVN 356

Query 360 GNLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSSKSCSDTSNSRASLTWCQRISMAVDV 419
GNLVKLMGVSSDN+GNCFFVVEYAENGSLDEWLFSS+ S TSNS SLTW QRI++AVDV
Sbjct 357 GNLVKLMGVSSDNEGNCFLVVEYAENGSLDEWLFSE-LSKTSNSVSLTWSQRITVAVDV 415

Query 420 AMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVV 479
A+GLQYMHEH YPRI+HRDIT+SNILLDSNFKAKIANFSMART TN MMPKIDVFAFGVV
Sbjct 416 AVGLQYMHEHTYPRIIHRDITTSNILLDSNFKAKIANFSMARTSTNPMMPKIDVFAFGVV 475

Query 480 LIELLTGRKAMTTKENGVEVWLWKDIWKIFDQENREERLKKWMDPKLESYYPIDYALSL 539
LIELLTG+KA+TT ENGVEV+LWKD WKIFD E NREE L+KWMMDPKLE++YPID ALSL
Sbjct 476 LIELLTGKKAITTMENGVEVVLWKDFWKIFDLEGNREESLRKWMMDPKLENFYPIDNALS 535

Query 540 ASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSA-TLERSLTSSGLDVEAT+QIVTSAIA 598
ASLAVNCTADKSLSRP+IAEIVL LSL L Q S LERSLT SGLDVEAT +VTSI AR
Sbjct 536 ASLAVNCTADKSLSRPSIAEIVLCLSLNQSSEPMLESLT-SGLDVEATHVVTISIVAR 594

>emb|CAE02597.1|  Nod-factor receptor 5 [Lotus japonicus]
emb|CAE02598.1|  Nod-factor receptor 5 [Lotus japonicus]
Length=595

GENE ID: 100034751 NFR5 | Nod-factor receptor 5 [Lotus japonicus]
(10 or fewer PubMed links)

Score = 875 bits (2262), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 449/601 (74%), Positives = 500/601 (83%), Gaps = 9/601 (1%)

Query 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETVVTYIAQSPN 60
MAVFF L S L L + L TNI A+S++ + +FSCP DSPSCETVVTY AQSPN
Sbjct 1 MAVFF--LTSGSLSLFLALTLLFTNIAARSEKISGPDFSCFPVDSPPSCETVVTYTAQSPN 58

Query 61 FLSLTNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQ 120
LSLTNIS+IFD SPLSIARASN++ DKL V QVLLVPVTCG GN S AN SY+I
Sbjct 59 LLSLTNISDIFDISPLSIARASNIDAGKDKLVPGQVLLVPVTCGACGNHSSANTSYQIL 118

Query 121 GDSFYFVATTSYENLTNWRVMDLNPVLSPNKLPFIGIQVVFPLFCCKPSKNQLDKEIKYL 180
GDS+ FVATT YENLTNW V NP ++P LP ++VVFPLFC+CPSPKNQL+K I+YL
Sbjct 119 GDSYDFVATTLYENLTNWNIVQASNPVNPVLLPERVKVVFPLFCRCPSKNQLNKGQYL 178

Query 181 ITYVWKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLPVTRLPVLARSPSDG 240
ITYVWKP DNVSLVS KFGASP DI++EN YGQ+FTAA NLP+LIPVT+LP L + S+G
Sbjct 179 ITYVWKPNDNVSLVSAKFGASPADILTENRYGQDFTAAATNLPILIPVTQLPELTQPSNG 238

Query 241 RKGGRILPVIIGISLGLCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYV 300
RK I L VI+GI+LGCTLL VL LVYVYC + K LNR+ASSAETADKLLSGVSGYV
Sbjct 239 RKSSIHLLVILGITLGLCTLLTAVLTGTLVYVYCRKKALNRTASSAETADKLLSGVSGYV 298

Query 301 SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKE-DVTEELKILQKVN 359
SKP +YE D IMEAT + S++CK+GESVYKANIEG+V+AVK+ KE EELKILQKVN
Sbjct 299 SKPNVYIIDIIMEATKDFSDCKVGEVYKANIEGRVAVKKIEGGANEELKILQKVN 358

Query 360 GNLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSSKSCSDTSNSRASLTWCQRISMAVDV 419
GNLVKLMGVSS DGNCF+VVEYAENGSL EWLFSKS S T N SLTW QRIS+AVDV
Sbjct 359 GNLVKLMGVSSGVDGNCFLVVEYAENGSLAEWLFSKS-SGTPN---SLTWSQRISIAVDV 414

Query 420 AMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVV 479
A+GLQYMHEH YPRI+HRDIT+SNILLDSNFKAKIANF+MART TNPMMPKIDVFAFGV+
Sbjct 415 AVGLQYMHEHTYPRIIHRDITTSNILLDSNFKAKIANFAMARTSTNPMMPKIDVFAFGVL 474

Query 480 LIELLTGRKAMTTKENGVEVWLWKDIWKIFDQENREERLKKWMDPKLESYYPIDYALSL 539
LIELLTGRKAMTTKENGVEVWLWKD+W+ IFD EENREER++KWMMDP LES+Y ID ALSL
Sbjct 475 LIELLTGRKAMTTKENGVEVWLWKDMWEIFDIEENREERIRKWMMDPNLESFYHIDNALS 534

Query 540 ASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSA-ATLERSLTSSGLDVE-ATQIVTSAIA 597
ASLAVNCTADKSLSRP++AEIVLSLS LTQ S TLERSLTSSGLDVE IVTSI A
Sbjct 535 ASLAVNCTADKSLSRPSMAEIVLSLSFLTQSSNPTLERSLTSSGLDVEDDAHIVTSITA 594

Query 598 R 598
Sbjct 595 R 595

>gb|ABF50224.1| Nod factor perception protein [Medicago truncatula]
Length=595

Score = 864 bits (2232), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 429/577 (74%), Positives = 485/577 (84%), Gaps = 6/577 (1%)

Query	24	TNIVAQSQQDNRTNFSCPSDPPSCETYVITYIAQSPNFLSLTNISNIFDTSPLSIARASN	83
		TNI AQ + TNF+CP DSPSCETYV Y AQSPNFLSL+NIS+IF+ SPL IA+ASN	
Sbjct	23	TNISAQPLYISETNFTCFVDSPPSCETYVAYRAQSPNFLSLSNISDIFNLSPLRIAKASN	82
Query	84	LEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSFYFVATTSYENLTNWRAVMD	143
		+E D KL+ DQ+LLVPVTCGCT N SFANI+Y I QGD+F+ ++ TSY+NLTN+ +	
Sbjct	83	IEAEDKKLIPDQLLLVPVTCGCTKNHSFANITYSIKQGDNFFILSITSYQNLTNYLEFKN	142
Query	144	LNPVLSPNKLPIGIQVVFPLFCCKPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPE	203
		NP LSP LP+ +V PLFCCKPSKNQL+K IKYLITYVW+ DNV+LVS KFGAS	
Sbjct	143	FNPNLSPDLLPLDTKVSVPFLFCCKPSKNQLNKGIKYLITYVWQDNDNVTLVSSKFGASQV	202
Query	204	DIMSNNYGQNFATAANNLPVLI PVTRLPVLARSPSDGRKGGIR-LPVIIGISLGCTLLVL	262
		+++ENN+ NFTA+ N VLI PVT LP L + S+GRK + L +IIIGISLG +L	
Sbjct	203	EMLAENNH--NFTASTNRSVLI PVTSLPKLDQSSNGRKSSSQNLALIIGISLGSAFFIL	260
Query	263	VLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQC	322
		VL + LVYVYCLMKM LNRS SS+ETADKLLSGVSGYVSKPTMYE DAIME T NLS+ C	
Sbjct	261	VLTLSLVYVYCLMKMRLNRSTSSSETADKLLSGVSGYVSKPTMYEIDAIMEGTTNLSNDC	320
Query	323	KIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNNLVKLMGVSSDNDGNCFFVVEY	382
		KIGESVYKANI+G+VLAVK+ K+D +EELKILQKVNHGNNLVKLMGVSSDNDGNCFF+VVEY	
Sbjct	321	KIGESVYKANIDGRVLAVKKIKKDAEELKILQKVNHGNNLVKLMGVSSDNDGNCFLVVEY	380
Query	383	AENGSLDEWLFSSKSDTSNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSS	442
		AENGSL+EWLFS+S S TSNS SLTW QRI++A+DVA+GLQYMHEH YPRI+HRDIT+S	
Sbjct	381	AENGSLDEWLFSES-SKTSNSVSLTWSQRIITIAMDVAIGLQYMHEHTYPRIIHRDITTS	439
Query	443	NILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVLIELLTGRKAMTTKENGVEVWLW	502
		NILL SNFKAKIANF MART TN MPMKIDVFAFGVVLIELLTG+KAMTTKENGVEV+LW	
Sbjct	440	NILLGSNFKAKIANFGMARTSTNSMMPKIDVFAFGVVLIELLTGKKAMTTKENGVEVILW	499
Query	503	KDIWKIFDQENREERLKKWMDPKLESYYPIDYALSLASLAVNCTADKSLSRPTIAEIVL	562
		KD WKIFD E NREERL+KWMMPKLES+YPID ALSLASLAVNCTADKSLSRPTIAEIVL	
Sbjct	500	KDFWKIFDLEGNREERLRKWMMPKLESFYPIDNALSASLAVNCTADKSLSRPTIAEIVL	559
Query	563	LSLLTQPSPA-TLERSLTSSGLDVEATQIVTSIAAR 598	
		LSLL QPS LERSLT SGLD EAT +VTS+ AR	
Sbjct	560	CLSLLNQPSSEPMLESLT-SGLDAEATHVVTSVIAR 595	

>emb|CA002956.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
Length=498

Score = 761 bits (1966), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 370/497 (74%), Positives = 423/497 (85%), Gaps = 4/497 (0%)

Query	46	PSCTEYVITYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGC	105
		PSCTEYV Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLVPVTCGC	
Sbjct	4	PSCTEYVAYRAQSPNFLSLSNISDIFNLSPLRIAKASNIEAEDKKLIPDQLLLVPVTCGC	63
Query	106	TGNRSFANISYEINQGDSFYFVATTSYENLTNWRAVMDLNPVLSPNKLPIGIQVVFPLFC	165
		T N SFANI+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFC	
Sbjct	64	TKNHSFANITYSIKQGDNFFILSITSYQNLTNYLEFKNFNPNLSPDLLPLDTKVSVPFLFC	123
Query	166	KCPSPNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSNNYGQNFATAANNLPVLI	225
		KCPSPNQL+K IKYLITYVW+ DNV+LVS KFGAS +++ENN+ NFTA+ N VLI	
Sbjct	124	KCPSPNQLNKGIKYLITYVWQDNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLI	181
Query	226	PVTRLPVLARSPSDGRKGGIR-LPVIIGISLGCTLLVLVLA VLLVYVYCLMKMTLNRSAS	284
		PVT LP L + S+GRK + L +IIIGISLG +LVL + LVYVYCLMKM LNRS S	
Sbjct	182	PVTSLPKLDQSSNGRKSSSQNLALIIGISLGSAFFILVLTLSLVYVYCLMKMRLNRSTS	241
Query	285	SAETADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFK	344
		S+ETADKLLSGVSGYVSKPTMYE DAIME TMNLS+ CKIGESVYKANI+G+VLAVK+ K	
Sbjct	242	SSETADKLLSGVSGYVSKPTMYEIDAIMEGTMNLSNCKIGESVYKANIDGRVLAVKKIK	301
Query	345	EDVTEELKILQKVNHGNNLVKLMGVSSDNDGNCFFVVEYEAENGSLDEWLFSSKSDTSNSR	404
		+D +EELKILQKVNHGNNLVKLMGVSSDNDGNCFF+VVEYEAENGSL+EWLFS+S S TSNS	
Sbjct	302	KDASEELKILQKVNHGNNLVKLMGVSSDNDGNCFLVVEYEAENGSLDEWLFSES-SKTSNSV	360
Query	405	ASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFT	464
		SLTW QRI++A+DVA+GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART T	
Sbjct	361	VSLTWSQRIITIAMDVAIGLQYMHEHTYPRIIHRDITTSNILLGSNFKAKIANFGMARTST	420
Query	465	NPMMPKIDVFAFGVVLIELLTGRKAMTTKENGVEVWLWKDIWKIFDQENREERLKKWMD	524
		N MPMKIDVFAFGVVLIELLTG+KAMTTKENGVEV+LWKD WKIFD E NREERL+KWMMD	
Sbjct	421	NSMMPKIDVFAFGVVLIELLTGKKAMTTKENGVEVILWKDFWKIFDLEGNREERLRKWMMD	480
Query	525	PKLESYYPIDYALSLAS 541	
		PKLES+YPID ALS+AS	
Sbjct	481	PKLESFYPIDNALSMAS 497	

>emb|CA002958.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
Length=492

Score = 754 bits (1948), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 367/494 (74%), Positives = 420/494 (85%), Gaps = 4/494 (0%)

Query	49	ETYVITYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGN	108
		ETYV Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLVPVTCGCT N	
Sbjct	1	ETYVAYRAQSPNFLSLSNISDIFNLSPLRIAKASNIEAEDKKLIPDQLLLVPVTCGCTKN	60
Query	109	RSFANISYEINQGDSFYFVATTSYENLTNWRAVMDLNPVLSPNKLPIGIQVVFPLFCCKP	168
		SFANI+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCCKP	
Sbjct	61	HSFANITYSIKQGDNFFILSITSYQNLTNYLEFKNFNPNLSPDLLPLDTKVSVPFLFCCKP	120
Query	169	SKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSNNYGQNFATAANNLPVLI PVT	228

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Sbjct 121 SKNQL+K IKYLITYVW+ DNV+LVS KFGAS ++++ENN+ NFTA+ N VLIPVT 178
          SKNQLNKGIKYLITYVWQDNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPT
Query 229 RLPVLARSPPSDGRKGGR-LPVIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAE 287
          LP L + S+GRK + L +IIGISLG +LVL + LVYVYCLMK LNRS SS+E
Sbjct 179 SLPKLDQPSSNGRKRSSSQNLALIIGISLGSAFFILVLTLSLVYVYCLMKRLNRSTSSSE 238
Query 288 TADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDV 347
          TADKLLSGVSGYVSKPTMYE DAIME TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D
Sbjct 239 TADKLLSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDA 298
Query 348 TEELKILQKVNHGNNLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSKSCSDTSNSRASL 407
          +EELKILQKVNHGNNLVKLMGVSSDNDGNCFF+VVEYAENGSL+EWLFS+S S TSNS SL
Sbjct 299 SEELKILQKVNHGNNLVKLMGVSSDNDGNCFLVVEYAENGSLDEWLFS+S-SKTSNSVSVSL 357
Query 408 TWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPM 467
          TW QRI++A+DVA+GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART TN M
Sbjct 358 TWSQRIPIAMDVAIGLQYMHEHTYPRIIHRDITTSNILLGSNFKAKIANFGMARTSTNSM 417
Query 468 MPKIDVFAFGVVLIELLTGKAMTTKENGGEVVMWKDIWKIFDQEEENREERLKKWMDPKL 527
          MPKIDVFAFGVVLIELLTG+KAMTTKENGGEVV+LWKD WKIFD E NREERL+KWMDBPKL
Sbjct 418 MPKIDVFAFGVVLIELLTGKAMTTKENGGEVVILWKDFWKIFDLEGNREERLRKWMDBPKL 477
Query 528 ESYYPIDYALSLAS 541
          ES+YPID ALS+AS
Sbjct 478 ESFYPIDNALSMAAS 491

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>emb|CA002933.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002934.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002935.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
10 more sequence titles

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emb|CA002938.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002939.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002952.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. longiaculeata]
emb|CA002955.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002957.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002959.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002967.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002971.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002972.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
emb|CA002973.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
Length=487

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Score = 747 bits (1928), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 363/489 (74%), Positives = 416/489 (85%), Gaps = 4/489 (0%)

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Query 54 YIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFAN 113
          Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLVPVTCGCT N SFAN
Sbjct 1 YRAQSPNFLSLNSIDIFNLSPLRIAKASNIEAEDKKLIPDQLLLVPVTCGCTKNHSFAN 60
Query 114 ISYINQGDSEFYFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQL 173
          I+Y I QGD+FE+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCKCPSKNQL
Sbjct 61 ITYSIKQGDNFFILSITSYQNLTNYLEFKNFNPNLSPTLLPLDTKVSVPFLFCKCPSKNQL 120
Query 174 DKEIKYLITYVWKGPDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLFVL 233
          +K IKYLITYVW+ DNV+LVS KFGAS ++++ENN+ NFTA+ N VLIPVT LP L
Sbjct 121 NKGIKYLITYVWQDNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPTSLPKL 178
Query 234 ARSPSDGRKGGR-LPVIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKL 292
          + S+GRK + L +IIGISLG +LVL + LVYVYCLMK LNRS SS+ETADKL
Sbjct 179 DQPSNNGRKRSSSQNLALIIGISLGSAFFILVLTLSLVYVYCLMKRLNRSTSSSETADKL 238
Query 293 LSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 352
          LSGVSGYVSKPTMYE DAIME TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDAEELK 298
Query 353 ILQKVNHGNNLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSKSCSDTSNSRASLTWCQR 412
          ILQKVNHGNNLVKLMGVSSDNDGNCFF+VVEYAENGSL+EWLFS+S S TSNS SLTW QR
Sbjct 299 ILQKVNHGNNLVKLMGVSSDNDGNCFLVVEYAENGSLDEWLFS+S-SKTSNSVSVSLTWSQR 357
Query 413 ISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKID 472
          I++A+DVA+GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART TN MMPKID
Sbjct 358 ITIAMDVAIGLQYMHEHTYPRIIHRDITTSNILLGSNFKAKIANFGMARTSTNSMMPKID 417
Query 473 VFAGGVVLIELLTGKAMTTKENGGEVVMWKDIWKIFDQEEENREERLKKWMDPKLESYYP 532
          VFAGGVVLIELLTG+KAMTTKENGGEVV+LWKD WKIFD E NREERL+KWMDBPKLES+YP
Sbjct 418 VFAGGVVLIELLTGKAMTTKENGGEVVILWKDFWKIFDLEGNREERLRKWMDBPKLESFYP 477
Query 533 IDYALSLAS 541
          ID ALS+AS
Sbjct 478 IDNALSMAAS 486

```

```

>emb|CA002951.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
Length=487

```

Score = 745 bits (1924), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 363/489 (74%), Positives = 415/489 (84%), Gaps = 4/489 (0%)

```

Query 54 YIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFAN 113
          Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLVPVTCGCT N SFAN
Sbjct 1 YRAQSPNFLSLNSIDIFNLSPLRIAKASNIEAEDKKLIPDQLLLVPVTCGCTKNHSFAN 60

```

```

Query 114 ISYEINQGDSEFYFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQL 173
          I+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCKCPSKNQL
Sbjct 61 ITYSIKQGDNFFILSITSYQNLNTYLEFKNFNPNLSPTLLPLDTKVSVPFLFCKCPSKNQL 120

Query 174 DKEIKYLITYVWKPGDNVSLVSKFGASPEDIMSENNYQGNFTAANNLPVLIIPVTRLFVL 233
          +K IKYLITYVW+ DNV+LVS KFGAS ++++ENN+ NFTA+ N VLIPVT LP L
Sbjct 121 NKGIKYLITYVWQDNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLI PVTSLPKL 178

Query 234 ARSPSDGRKGGR-LPVIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKL 292
          + S+GRK + L +IIGISLG +LVL + LVYVYCLMK LNRS SS+ETADKL
Sbjct 179 DQPSNNGRKGSSQNLAIIIGISLGAFFILVLTLSLVYVYCLMKRLNRSSTSSSETADKL 238

Query 293 LSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 352
          LSGVSGYVSKPTMYE DAIME T NLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTTNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK 298

Query 353 ILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSKSCSDTSNSRASLTWCQR 412
          ILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSL+EWLFS+S TSNS SLTW QR
Sbjct 299 ILQKVNHNGLVKLMGVSSDNDGNCFLVVEYAENGSLDEWLFSSES-SKTSNSVSLTWSQR 357

Query 413 ISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKID 472
          I++A+DVA+GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART TN MMPKID
Sbjct 358 ITIAMDVAIGLQYMHEHTYPRIIHRDITTSNILLGSNFKAKIANFGMARTSTNSMMPKID 417

Query 473 VFAPGVVLIELLTGKAMTTKENGGEVVLWKDIWKIFDQENREERLKKWMDPKLESYYP 532
          VFAPGVVLIELLTG+KAMTTKENGGEV+LWKD WKIFD E NREERL+KWMDPKLES+YP
Sbjct 418 VFAPGVVLIELLTGKAMTTKENGGEVVLWKDFWKIFDLEGNREERLRKWMDPKLESFYF 477

Query 533 IDYALSLAS 541
          ID ALSLAS
Sbjct 478 IDNALSLAS 486

```

>**emb|CA002940.1** | LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=487

Score = 745 bits (1923), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 363/489 (74%), Positives = 415/489 (84%), Gaps = 4/489 (0%)

```

Query 54 YIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFAN 113
          Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLVPVTCGCT N SFAN
Sbjct 1 YRAQSPNFLSLSNISDIFNLSPRIAKASNIEAEDKKLIPDQLLLVPTVTCGCTKNHSFAN 60

Query 114 ISYEINQGDSEFYFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQL 173
          I+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCKCPSKNQL
Sbjct 61 ITYSIKQGDNFFILSITSYQNLNTYLEFKNFNPNLSPTLLPLDTKVSVPFLFCKCPSKNQL 120

Query 174 DKEIKYLITYVWKPGDNVSLVSKFGASPEDIMSENNYQGNFTAANNLPVLIIPVTRLFVL 233
          +K IKYLITYVW+ DNV+LVS KFGAS ++++ENN+ NFTA+ N VLIPVT LP L
Sbjct 121 NKGIKYLITYVWQDNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLI PVTSLPKL 178

Query 234 ARSPSDGRKGGR-LPVIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKL 292
          + S+GRK + L +IIGISLG +LVL + LVYVYCLMK LNRS SS+ETADKL
Sbjct 179 DQPSNNGRKGSSQNLAIIIGISLGAFFILVLTLSLVYVYCLMKRLNRSSTSSSETADKL 238

Query 293 LSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 352
          LSGVSGYVSKPTMYE DAIME TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK 298

Query 353 ILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSKSCSDTSNSRASLTWCQR 412
          ILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSL+EWLFS+S TSNS SLTW QR
Sbjct 299 ILQKVNHNGLVKLMGVSSDNDGNCFLVVEYAENGSLDEWLFSSEWK-TSNSVSLTWSQR 357

Query 413 ISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKID 472
          I++A+DVA+GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART TN MMPKID
Sbjct 358 ITIAMDVAIGLQYMHEHTYPRIIHRDITTSNILLGSNFKAKIANFGMARTSTNSMMPKID 417

Query 473 VFAPGVVLIELLTGKAMTTKENGGEVVLWKDIWKIFDQENREERLKKWMDPKLESYYP 532
          VFAPGVVLIELLTG+KAMTTKENGGEV+LWKD WKIFD E NREERL+KWMDPKLES+YP
Sbjct 418 VFAPGVVLIELLTGKAMTTKENGGEVVLWKDFWKIFDLEGNREERLRKWMDPKLESFYF 477

Query 533 IDYALSLAS 541
          ID ALSLAS
Sbjct 478 IDNALSLAS 486

```

>**emb|CA002941.1** | LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
>**emb|CA002970.1** | LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=487

Score = 744 bits (1922), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 362/489 (74%), Positives = 415/489 (84%), Gaps = 4/489 (0%)

```

Query 54 YIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFAN 113
          Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLVPVTCGCT N SFAN
Sbjct 1 YRAQSPNFLSLSNISDIFNLSPRIAKASNIEAEDKKLIPDQLLLVPTVTCGCTKNHSFAN 60

Query 114 ISYEINQGDSEFYFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQL 173
          I+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCKCPSKNQL
Sbjct 61 ITYSIKQGDNFFILSITSYQNLNTYLEFKNFNPNLSPTLLPLDTKVSVPFLFCKCPSKNQL 120

Query 174 DKEIKYLITYVWKPGDNVSLVSKFGASPEDIMSENNYQGNFTAANNLPVLIIPVTRLFVL 233
          +K IKYLITYVW+ DNV+LVS KFGAS ++++ENN+ NFTA+ N VLIPVT LP L
Sbjct 121 NKGIKYLITYVWQDNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLI PVTSLPKL 178

Query 234 ARSPSDGRKGGR-LPVIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKL 292
          + S+GRK + L +IIGISLG +LVL + LVYVYCLMK LNRS SS+ETADKL
Sbjct 179 DQPSNNGRKGSSQNLAIIIGISLGAFFILVLTLSLVYVYCLMKRLNRSSTSSSETADKL 238

Query 293 LSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 352
          LSGVSGYVSKPTMYE DAIME T NLS+ CKIGESVYKAN++G+VLAVK+ K+D +EELK
Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTTNLSDNCKIGESVYKANMDGRVLAVKKIKKDASEELK 298

Query 353 ILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSKSCSDTSNSRASLTWCQR 412

```

Sbjct	299	ILQKVNHNGLVKLMGVSSDNDGNCFLVYEYAENGSL+EWLFS+S S TSNS SLTW QR ILQKVNHNGLVKLMGVSSDNDGNCFLVYEYAENGSL+EWLFS+S S TSNS SLTW QR	357
Query	413	ISMAVDVAMGLQYMHEHAYPRI+VRHDITSSNILLDSNFKAKIANFSMARTFTNPMMPKID I+H+DVA+GLQYMHEH YPRI+VRHDITSSNILLDSNFKAKIANF MART TN PMMPKID	472
Sbjct	358	ITIAMDVAIGLQYMHEHTYPRIIHRDITSSNILLGSNFKAKIANFGMARTSTNSMMPKID	417
Query	473	VFAFGVVLIELLTGRKAMTTKENGVEVWLWWDIKWIFDQENREERLKKWMDPKLESYP VFAFGVVLIELLTG+KAMTTKENGVEV+LWWD WKIFD E NREERL+K+WMDDPKLES+YP	532
Sbjct	418	VFAFGVVLIELLTGKKAMTTKENGVEVWLWWDIKWIFDLEGNREERLKKWMDPKLESFYP	477
Query	533	IDYALSLAS 541 ID ALSLAS	
Sbjct	478	IDNALSLAS 486	

>emb|CA002966.1| LysM-domain containing receptor-like kinase [Medicago tornata]
Length=487

Score = 741 bits (1914), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 362/489 (74%), Positives = 414/489 (84%), Gaps = 4/489 (0%)

Query	54	YIAQSPNFLSLSTNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFAN	113
Sbjct	1	Y AQSPNFLSL+NIS+IF+ SPL IAA+ASN+E D KL+DQ+LLVPVTCGCT N SFAN YIAQSPNFLSLSLNIDIFNLSPLRIAKASNIABEDKLIPDQLLVPVTCGCTKNHSFAN	60
Query	114	ISYEINQGDSFYFVATTSYENLTNWRAVMDLNPVLSPNKLPIGIQVFPFCKCPSKNQL	173
Sbjct	61	I+Y I GD+P+ ++ TSY+NLNTN+ + NP LSP L+ + V PLEFCCKPSKNQL ITYTSIKLGDGPFILSTSYQNLTNYLEFKNPLSLPTLLPDLTKVSVLPFCKCPSKNQL	120
Query	174	DKEIKYLITYVWVKQDNVLSVSKFGASPEDIMSENNGQNFTAANNLPVLIPTVTRLPVL	233
Sbjct	121	+K IXYLTITYVW+ DNV+LVS KFGAS +++ENNT+ NFTA+ N VLIPTP LP L NKGIXLYLTITYVWQDNDNVLISLISGFGASQVMEALENN--NFTASTNRSVLIPVTSLPKL	178
Query	234	ARSPSDGRKGGR-LPVIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKL	292
Sbjct	179	+ S+GRK + L +IIGISLG +LVL+ LVVYVYCLMK LNRS SS+ETADKL DQPSNDRKRSSQNSALIDIGISLGSFAFILLVLTLSLVYVYCLMKMRLNRTSSSETADKL	238
Query	293	LSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEVDTEELK	352
Sbjct	239	LSGVSGYVSKPTMYE DAIME TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK LSGVSGYVSKPTMYEIDAIMEGMTMNLSDNCKIGESVYKANIDGRVLAVKKIKDAEELK	298
Query	353	ILQKVHNHGNLVKLMGVSSDNDGNCFFVYEYEAENGSLDEWLFSKSCSDTNSNRASLTWCQR	412
Sbjct	299	ILQKVHNHGNLVKLMGVSSDNDGNCFF+VYEYEAENGSL+EWLFS+S S TSNS SL+W QR ILQKVHNHGNLVKLMGVSSDNDGNCFFLVYEYEAENGSLDEWLFS+S-SKTNSNVSVLSWSQR	357
Query	413	ISMAVDVAMGLQYMHCHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKID	472
Sbjct	358	I++A+DVA+GLQYMHCH YPRI+HRDIT+SNILL SNFKAKIANF MART TN MPMKID TIAMDAIGLQYMHCHTYPRI IHRDITTSNILLGSNFKAKIANFGMARTSTNSMMPKID	417
Query	473	VFAFGVLLIELLTGRKAMTTKENGVEVWLWKD IWKIFDQEENREERLKKWMDPKLESYYP	532
Sbjct	418	VFAFGVLLIELLTG+KAMTTKENGVEV+LWKD WKIFD E NREERL KWMMDPKLES+YYP VFAFGVLLIELLTGKKAMTTKENGVEV+LWKDFWKIFDLEGNRERLKKWMDPKLESFYYP	477
Query	533	IDYALSLAS 541	
Sbjct	478	ID ALSLAS IDNALSLAS 486	

```
>dbj|BAI79275.1| LysM type receptor kinase [Lotus japonicus]
```


dbj|BAI79285.1| LysM type receptor kinase [Lotus japonicus]
Length=591

GENE ID: 100380877 **LYS11** | LysM type receptor kinase [Lotus japonicus]
(10 or fewer PubMed links)

Score = 704 bits (1817), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 376/606 (62%), Positives = 461/606 (76%), Gaps = 23/606 (3%)

Query	1	MAVFFFFPLPLHSQILCLVIMLFST--NIVAQSQQDNRTNFSCPSDSPSCETYTYTYIAQS	58
Sbjct	1	M FF F + + + ++M FST ++IAQ N TNFSCP DSPSPCD+TYTYTY AQS MTSFFLFT---NTLFLAIIIMMFSTTHHILAQLSHTNGTNFSCVPDSPSCDYTYTYTFAQS	57
Query	59	PNFLSLTNISNIFDTPSLSIARASNLEPMDDKLVKDVQLLVPVTCGCTGNRSFANISYEI	118
Sbjct	58	PNFL+LT+IS++FDTSPSLSIARASN++ + LV Q+LLVPVTC C+G+ SF+NIS+ I PNFLTLTGISLDLFTSPSLSIARASNIDEN+LVLPGQLLVPVFLCACSGSNFNSISHMI	118
Query	119	NQGDSEFYFVATTSEYENLTNWRAVMDLNPVLSPNKLPIGIVQVFLPCKCPSKNQLDKKIK	178
Sbjct	118	+G+S+Y+++TTSYENLTNW V D NP + P LP+GI+V FLPCFKPS L+K+I KEGESYYLSTSEYENLTNWETVQDSNPENYPYLLPGVIGVVIPLFCPCPSNYHLNGIE	177
Query	179	YLITYVWKPGDENVSLVSKFGASPEDIMSENNYG-QNFTAANNLPLVLIPTVTRLPLVLARSP	237
Sbjct	178	YLITYVW DNVSLV+ KFG S +DI+SENN+ QNFATAA N P+LIPVTL+LP L+S+S YLITYVWHNNDNVSLVASKFGVSTQDIISENNFSHQNFATAATNPFLIPVTLPLSPLSQSY	237
Query	238	SDGRGGIRLPVIGISLGC TTLVLVLAVL-LVYVYCLMKM--TLNRSASSAETA-DKLL	293
Sbjct	238	S + II L+ +A+L LV V CL+ + + N+S S E A KL+ SSSERKRNSNHIIHIIISIGISLGSTLLIALLVLVSVTCLRKRKSSSENKSLLSVEIAGKKLI	297
Query	294	SGVSGYVSKPTMYETDAIMEATNLNLEQCKIGESVYKANIEGKVLAVKRFKDEDTEELKI	353
Sbjct	298	SGVS YVSK +YE I MEAT+M+LEQCKIGESVYKA ++G+VLAVK+ KEDVTEB+ I SGVSNVYSKSLIYEFRLIMEAT+LNLNEQCKIGESVYKAKLDGQVLAVKKVKEDVTEEVMI	357
Query	354	LQKVHNHGNLVKLMGVSSDNDGNCVFVVEYEAENGSLDEWLFSSKCSKSDTSNRSASLTWCQRI	413
Sbjct	358	LQKVNH NLVKLMGVSS +DGN F+VYE+AEENGSL WLF S ++ SR LTW QRI LQKVHNHNLNLVKLMGVSSGHDGNHFLIYVEFAENGSLHNWLFNS-- -STGSRF-LTWQRI	413
Query	414	SMADVAVMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTTNMMPKIDV	473
Sbjct	414	SMAVDVAMGLQYMHEH P I VHRDITSSNILLDSNFKAKIANFS+ART NPM+ K+DV SIADVAVMGLQYMHEHTQPSIVHRDITSSNILLDSNFKAKIANFSVARTSNINPMILKVDV	473
Query	474	FAFGVVLLELTGRKAMTTKKEGNEVVMWKDIWKIFQEEENREERLLKWMDPKLESYYPI	533
Sbjct	474	F+GVVLE+ELL+G+K+X+T N E+ I +IFD +E REER++WMDPK+ES YPI FGYGVVLELLELSGKKSLT---NNEI----NHIREIFDLKEKREERIRRWMPDKIESLYPI	526
Query	534	DYALSLASLAVNTADKLSLRPTTAEIVLSLSLL-LTPQSPATTLERSLTSSGSLDVEATQIV	592
Sbjct	534	D ALSIA LA+NCT++K LSRPT+ E+VLSLSLL TO SP.TLERS T GLD+V T++ DALSIA LA+NCT++K LSRPT+ E+VLSLSLL TO SP.TLERS T GLD+V T++	592

```
Sbjct 527 DDALSLAFLAMNCTSEKPLSRPTMGEVVLSSLMLTQHSPTTLERSWT-CGLDQVDMTEMQ 585
Query 593 TSIAAR 598
          T IAAR
Sbjct 586 TLIAAR 591
```

>gb|ADJ19109.1|  truncated Nod-factor receptor 5A [Glycine max]
Length=337

GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
(10 or fewer PubMed links)

```
Score = 695 bits (1793), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 337/337 (100%), Positives = 337/337 (100%), Gaps = 0/337 (0%)

Query 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPPCSETYVVTYIAQSPN 60
Sbjct 1 MAVFFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPPCSETYVVTYIAQSPN 60

Query 61 FLSLTNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQ 120
Sbjct 61 FLSLTNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQ 120


Query 121 GDSFYFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYL 180
Sbjct 121 GDSFYFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYL 180

Query 181 ITYVWKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDG 240
Sbjct 181 ITYVWKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDG 240

Query 241 RKGIRLPVLIIGISLGCTLLVLVAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYV 300
Sbjct 241 RKGIRLPVLIIGISLGCTLLVLVAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYV 300

Query 301 SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKV 337
Sbjct 301 SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKV 337
```

>dbj|BAG85143.1| Nod factor receptor protein [Glycine soja]
dbj|BAG85149.1| Nod factor receptor protein [Glycine soja]
dbj|BAG85156.1| Nod factor receptor protein [Glycine soja]
11 more sequence titles

dbj|BAG85159.1| Nod factor receptor protein [Glycine max]
dbj|BAG85160.1| Nod factor receptor protein [Glycine max]
dbj|BAG85161.1| Nod factor receptor protein [Glycine max]
dbj|BAG85162.1| Nod factor receptor protein [Glycine max]
dbj|BAG85165.1| Nod factor receptor protein [Glycine max]
dbj|BAG85168.1| Nod factor receptor protein [Glycine max]
dbj|BAG85171.1| Nod factor receptor protein [Glycine max]
dbj|BAG85174.1| Nod factor receptor protein [Glycine max]
dbj|BAG85177.1|  Nod factor receptor protein [Glycine max]
dbj|BAG85179.1| Nod factor receptor protein [Glycine max]
dbj|BAG85180.1| Nod factor receptor protein [Glycine max]
Length=327

```
Score = 675 bits (1741), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 327/327 (100%), Positives = 327/327 (100%), Gaps = 0/327 (0%)

Query 5 FFFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPPCSETYVVTYIAQSPNFLSL 64
Sbjct 1 FFFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPPCSETYVVTYIAQSPNFLSL 60

Query 65 TNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQGDSE 124
Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQGDSE 120

Query 125 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 184
Sbjct 121 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180

Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 244
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 240

Query 245 IRLPVIIGISLGCTLLVLVAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 304
Sbjct 241 IRLPVIIGISLGCTLLVLVAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
```

>dbj|BAG85148.1| Nod factor receptor protein [Glycine soja]
Length=327

```
Score = 674 bits (1739), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 327/327 (100%), Gaps = 0/327 (0%)

Query 5 FFFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPPCSETYVVTYIAQSPNFLSL 64
Sbjct 1 FFFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPPCSETYVVTYIAQSPNFLSL 60

Query 65 TNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQGDSE 124
Sbjct 61 TNISNIFDTSPLSVARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEINQGDSE 120

Query 125 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 184
Sbjct 121 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180

Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 244
          WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG
```

```
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 240
Query 245 IRLPVIIGISLGLCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 304
          IRLPVIIGISLGLCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPVIIGISLGLCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
          MYETDAIMEATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
```

>dbj|BAG85151.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 673 bits (1736), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 327/327 (100%), Gaps = 0/327 (0%)

```
Query 5 FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL 64
          FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL
Sbjct 1 FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL 60


Query 65 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE 124
          TNISNIF+TSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE
Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE 120

Query 125 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 184
          YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV
Sbjct 121 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180

Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 244
          WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 240

Query 245 IRLPVIIGISLGLCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 304
          IRLPVIIGISLGLCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPVIIGISLGLCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
          MYETDAIMEATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
```

>dbj|BAG85178.1|  Nod factor receptor protein [Glycine max]
Length=327

GENE ID: 100498858 NFR5a | Nod-factor receptor 5A [Glycine max]
(10 or fewer PubMed links)

Score = 673 bits (1736), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 327/327 (100%), Gaps = 0/327 (0%)

```
Query 5 FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL 64
          FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL
Sbjct 1 FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL 60

Query 65 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE 124
          TNISNIFDT+PLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE
Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE 120

Query 125 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 184
          YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV
Sbjct 121 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180

Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 244
          WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 240

Query 245 IRLPVIIGISLGLCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 304
          IRLPVIIGISLGLCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPVIIGISLGLCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
          MYETDAIMEATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
```

>dbj|BAG85167.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 673 bits (1736), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

```
Query 5 FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL 64
          FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL
Sbjct 1 FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL 60

Query 65 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE 124
          NISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE
Sbjct 61 ANISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE 120

Query 125 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 184
          YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV
Sbjct 121 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180

Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 244
          WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 240

Query 245 IRLPVIIGISLGLCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 304
          IRLPVIIGISLGLCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPVIIGISLGLCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
          MYETDAIMEATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
```

>dbj|BAG85164.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 673 bits (1736), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query	5	FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPPCSETYVVTYIAQSPNFLSL	64
		FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPPCSETYVVTYIAQSPNFLSL	
Sbjct	1	FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPPCSETYVVTYIAQSPNFLSL	60
Query	65	TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF	124
		TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF	
Sbjct	61	TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF	120
Query	125	YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	184
		YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	
Sbjct	121	YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	180
Query	185	WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG	244
		WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG	
Sbjct	181	WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG	240
Query	245	IRLPVIIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT	304
		IRLPVIIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT	
Sbjct	241	IRLPVIIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT	300
Query	305	MYETDAIMEATMNLSEQCKIGESVYKA 331	
		MYE DAIMEATMNLSEQCKIGESVYKA	
Sbjct	301	MYEADAIMEATMNLSEQCKIGESVYKA 327	

>dbj|BAG85170.1| Nod factor receptor protein [Glycine max]
Length=327


Score = 672 bits (1735), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 327/327 (100%), Gaps = 0/327 (0%)

Query	5	FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPPCSETYVVTYIAQSPNFLSL	64
		FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPPCSETYVVTYIAQSPNFLSL	
Sbjct	1	FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPPCSETYVVTYIAQSPNFLSL	60
Query	65	TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF	124
		TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFA+ISYEINQGDSF	
Sbjct	61	TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFADISYEINQGDSF	120
Query	125	YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	184
		YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	
Sbjct	121	YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	180
Query	185	WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG	244
		WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG	
Sbjct	181	WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG	240
Query	245	IRLPVIIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT	304
		IRLPVIIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT	
Sbjct	241	IRLPVIIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT	300
Query	305	MYETDAIMEATMNLSEQCKIGESVYKA 331	
		MYETDAIMEATMNLSEQCKIGESVYKA	
Sbjct	301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>dbj|BAG85146.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 672 bits (1735), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 327/327 (100%), Gaps = 0/327 (0%)

Query	5	FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPPCSETYVVTYIAQSPNFLSL	64
		FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPPCSETYVVTYIAQSPNFLSL	
Sbjct	1	FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPPCSETYVVTYIAQSPNFLSL	60
Query	65	TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF	124
		TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF	
Sbjct	61	TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF	120
Query	125	YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	184
		YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	
Sbjct	121	YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	180
Query	185	WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG	244
		WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG	
Sbjct	181	WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG	240
Query	245	IRLPVIIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT	304
		IRLPVIIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT	
Sbjct	241	IRLPVIIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT	300
Query	305	MYETDAIMEATMNLSEQCKIGESVYKA 331	
		+YETDAIMEATMNLSEQCKIGESVYKA	
Sbjct	301	VYETDAIMEATMNLSEQCKIGESVYKA 327	

>dbj|BAG85158.1|  Nod factor receptor protein [Glycine max]
Length=327

GENE ID: 100301877 nfr5a | Nod factor receptor protein [Glycine max]
(10 or fewer PubMed links)

Score = 672 bits (1735), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query	5	FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPPCSETYVVTYIAQSPNFLSL	64
		FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPPCSETYVVTYIAQSPNFLSL	
Sbjct	1	FPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPPCSETYVVTYIAQSPNFLSL	60
Query	65	TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF	124


```
Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120
          TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF
Query 125 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 184
          YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV
Sbjct 121 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180
          YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV
Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYQNF TAANNLPVLI PVTRL PVLARSPSDGRKGG 244
          WKPGDNVSLVSDKFGASPEDIMSENNYQNF TAANNLPVLI PVTRL PVLARSPSDGRKGG
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNF TAANNLPVLI PVTRL PVLARSPSDGRKGG 240
          WKPGDNVSLVSDKFGASPEDIMSENNYQNF TAANNLPVLI PVTRL PVLARSPSDGRKGG
Query 245 IRLPVIIGISLGTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 304
          IRLPVIIGISLGTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPVIIGISLGTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 300
          IRLPVIIGISLGTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT
Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
          MYETDAIMEATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
          MYETDAIMEATMNLSEQCKIGESVYKA
```

>dbj|BAG85144.1| Nod factor receptor protein [Glycine soja]
>dbj|BAG85145.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 672 bits (1734), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

```
Query 5 FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL 64
          FFFPLPLH QILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL
Sbjct 1 FFFPLPLHFQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL 60
          FFFPLPLH FQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL
Query 65 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 124
          TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF
Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120
          TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF
Query 125 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 184
          YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV
Sbjct 121 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180
          YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV
Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYQNF TAANNLPVLI PVTRL PVLARSPSDGRKGG 244
          WKPGDNVSLVSDKFGASPEDIMSENNYQNF TAANNLPVLI PVTRL PVLARSPSDGRKGG
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNF TAANNLPVLI PVTRL PVLARSPSDGRKGG 240
          WKPGDNVSLVSDKFGASPEDIMSENNYQNF TAANNLPVLI PVTRL PVLARSPSDGRKGG
Query 245 IRLPVIIGISLGTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 304
          IRLPVIIGISLGTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPVIIGISLGTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 300
          IRLPVIIGISLGTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT
Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
          MYETDAIMEATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
          MYETDAIMEATMNLSEQCKIGESVYKA
```

>dbj|BAG85142.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 672 bits (1734), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

```
Query 5 FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL 64
          FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL
Sbjct 1 FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL 60
          FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL
Query 65 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 124
          TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF
Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120
          TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF
Query 125 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 184
          YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV
Sbjct 121 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180
          YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV
Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYQNF TAANNLPVLI PVTRL PVLARSPSDGRKGG 244
          WKPGDNVSLVSDKFGASPEDIMSENNYQNF TAANNLPVLI PVTRL PVLARSPSDGRKGG
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNF TAANNLPVLI PVTRL PVLARSPSDGRKGG 240
          WKPGDNVSLVSDKFGASPEDIMSENNYQNF TAANNLPVLI PVTRL PVLARSPSDGRKGG
Query 245 IRLPVIIGISLGTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 304
          IRLPVIIGISLGTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPVIIGISLGTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 300
          IRLPVIIGISLGTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT
Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
          MYETDAIMEATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
          MYETDAIMEATMNLSEQCKIGESVYKA
```

>dbj|BAG85152.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 672 bits (1733), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

```
Query 5 FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL 64
          FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL
Sbjct 1 FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL 60
          FFFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL
Query 65 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 124
          TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF
Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120
          TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF
Query 125 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 184
          YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV
Sbjct 121 YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180
          YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV
Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYQNF TAANNLPVLI PVTRL PVLARSPSDGRKGG 244
          WKPGDNVSLVSDKFGASPEDIMSENNYQNF TAANNLPVLI PVTRL PVLARSPSDGRKGG
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYQNF TAANNLPVLI PVTRL PVLARSPSDGRKGG 240
          WKPGDNVSLVSDKFGASPEDIMSENNYQNF TAANNLPVLI PVTRL PVLARSPSDGRKGG
Query 245 IRLPVIIGISLGTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 304
          IRLPVIIGISLGTLLV VLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPVIIGISLGTLLVQVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 300
          IRLPVIIGISLGTLLVQVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT
```

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
MYETDAIMEATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BAG85175.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 672 bits (1733), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 325/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVVTYIAQSPNFLSL 64
FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNF+CPSPSPSPSCETYVVTYIAQSPNFLSL
Sbjct 1 FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTKFTCPSPSPSPSCETYVVTYIAQSPNFLSL 60

Query 65 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 124
TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF
Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120

Query 125 YFVATTSYENLNTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 184
YFVATTSYENLNTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV
Sbjct 121 YFVATTSYENLNTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180

Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 244
WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 240

Query 245 IRLPVIIGISLGCTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 304
IRLPVIIGISLGCTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPVIIGISLGCTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
MYETDAIMEATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BAG85172.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 671 bits (1732), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVVTYIAQSPNFLSL 64
FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVVTYIAQSPNFLSL
Sbjct 1 FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVVTYIAQSPNFLSL 60

Query 65 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 124
TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF
Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120

Query 125 YFVATTSYENLNTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 184
YFVATTSYENLNTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV
Sbjct 121 YFVATTSYENLNTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180

Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 244
WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 240

Query 245 IRLPVIIGISLGCTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 304
IRLPVIIGISLGCTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPVIIGISLGCTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
MYETDAIMEATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BAG85157.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 671 bits (1732), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 326/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVVTYIAQSPNFLSL 64
FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVVTYIAQSPNFLSL
Sbjct 1 FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVVTYIAQSPNFLSL 60

Query 65 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 124
TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF
Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120

Query 125 YFVATTSYENLNTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 184
YFVATTSYENLNTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV
Sbjct 121 YFVATTSYENLNTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180

Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 244
WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 240

Query 245 IRLPVIIGISLGCTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 304
IRLPVIIGISLGCTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241 IRLPVIIGISLGCTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
MYETDAIMEATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327

>dbj|BAG85150.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 671 bits (1731), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 325/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)

Query 5 FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVVTYIAQSPNFLSL 64
FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVVTYIAQSPNFLSL
Sbjct 1 FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVVTYIAQSPNFLSL 60

Query	65	TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE	124
		TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE	
Sbjct	61	TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE	120
Query	125	YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	184
		YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	
Sbjct	121	YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	180
Query	185	WKPGDNVSLVSDKFGASPEDIMSENNYQNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	244
		WKPGDNVSLVSDKFGASPEDIMSENNYQNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	
Sbjct	181	WKPGDNVSLVSDKFGASPEDIMSENNYQNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	240
Query	245	IRLPVIGISLGCTLLVLVAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT	304
		IRLP IIGISLGCTLLVLVAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT	
Sbjct	241	IRLPAIIGISLGCTLLVLVAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT	300
Query	305	MYETDAIMEATMNLSEQCKIGESVYKA 331	
		MYETDAIMEATMNLSEQCKIGESVYKA	
Sbjct	301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>dbj|BAG85176.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 670 bits (1728), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 325/327 (99%), Positives = 326/327 (99%), Gaps = 0/327 (0%)

Query	5	FFFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL	64
		FFFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL	
Sbjct	1	FFFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL	60
Query	65	TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE	124
		TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE	
Sbjct	61	TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE	120
Query	125	YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	184
		YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	
Sbjct	121	YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	180
Query	185	WKPGDNVSLVSDKFGASPEDIMSENNYQNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	244
		WKPGDNVSLVSDKFGASPEDIMSENNYQNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	
Sbjct	181	WKPGDNVSLVSDKFGASPEDIMSENNYQNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	240
Query	245	IRLPVIGISLGCTLLVLVAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT	304
		IRLPVIGISLGCTLLVLVAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT	
Sbjct	241	IRLPVIGISLGCTLLVLVAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT	300
Query	305	MYETDAIMEATMNLSEQCKIGESVYKA 331	
		MYETDAIMEATMNLSEQCKIGESVYKA	
Sbjct	301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>dbj|BAG85153.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 669 bits (1727), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 325/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)

Query	5	FFFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL	64
		FFFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL	
Sbjct	1	FFFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL	60
Query	65	TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE	124
		TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE	
Sbjct	61	TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE	120
Query	125	YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	184
		YFVATTSYENLTNWRVMDLNPVLS NKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	
Sbjct	121	YFVATTSYENLTNWRVMDLNPVLSNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	180
Query	185	WKPGDNVSLVSDKFGASPEDIMSENNYQNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	244
		WKPGDNVSLVSDKFGASPEDIMSENNYQNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	
Sbjct	181	WKPGDNVSLVSDKFGASPEDIMSENNYQNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	240
Query	245	IRLPVIGISLGCTLLVLVAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT	304
		IRLPVIGISLGCTLLVLVAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT	
Sbjct	241	IRLPVIGISLGCTLLVLVAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT	300
Query	305	MYETDAIMEATMNLSEQCKIGESVYKA 331	
		MYETDAIMEAT NLSEQCKIGESVYKA	
Sbjct	301	MYETDAIMEATMNLSEQCKIGESVYKA 327	

>dbj|BAG85155.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 669 bits (1726), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 325/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)

Query	5	FFFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL	64
		FFFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL	
Sbjct	1	FFFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSL	60
Query	65	TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE	124
		TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE	
Sbjct	61	TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE	120
Query	125	YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV	184
		YFVAT SYENLTNWRVMDLNPVLSPNKLPIGIQV FFLFCKCPSKNQLDKEIKYLITYV	
Sbjct	121	YFVATPSYENLTNWRVMDLNPVLSPNKLPIGIQVEFPLFCKCPSKNQLDKEIKYLITYV	180
Query	185	WKPGDNVSLVSDKFGASPEDIMSENNYQNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	244
		WKPGDNVSLVSDKFGASPEDIMSENNYQNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	
Sbjct	181	WKPGDNVSLVSDKFGASPEDIMSENNYQNFTAANNLPVLIPVTRLPVLARSPSDGRKGG	240
Query	245	IRLPVIGISLGCTLLVLVAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT	304
		IRLPVIGISLGCTLLVLVAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT	

```
Sbjct 241 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKTlnrsassaetadkllsgvsgyvsKPT 300
Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
          MYETDAIMEATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
```

>dbj|BAG85163.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 669 bits (1726), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 325/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)

```
Query 5 FPFPLPHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVVTYIAQSPNFLSL 64
          FPFPLPHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSP SCETYV YIAQSPNFLSL
Sbjct 1 FPFPLPHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPASCETYVPYIAQSPNFLSL 60

Query 65 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 124
          TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF
Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120

Query 125 YFVATTSYENLNTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 184
          YFVATTSYENLNTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV
Sbjct 121 YFVATTSYENLNTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180

Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 244
          WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 240

Query 245 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKTlnrsassaetadkllsgvsgyvsKPT 304
          IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKTlnrsassaetadkllsgvsgyvsKPT
Sbjct 241 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKTlnrsassaetadkllsgvsgyvsKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
          MYETDAIMEATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
```

>dbj|BAG85173.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 669 bits (1725), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 325/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)

```
Query 5 FPFPLPHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVVTYIAQSPNFLSL 64
          FPFPLPHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVVTYIAQSPNFLSL
Sbjct 1 FPFPLPHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVVTYIAQSPNFLSL 60

Query 65 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 124
          TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF
Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120

Query 125 YFVATTSYENLNTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 184
          YFVATTSYENLNTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV
Sbjct 121 YFVATTSYENLNTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180

Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 244
          WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG
Sbjct 181 WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 240

Query 245 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKTlnrsassaetadkllsgvsgyvsKPT 304
          IRLPVIIGISLGCTLLVL LAVLLVYVYCLKMKTlnrsassaetadkllsgvsgyvsKPT
Sbjct 241 IRLPVIIGISLGCTLLVLGLAVLLVYVYCLKMKTlnrsassaetadkllsgvsgyvsKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
          MY TDAIMEATMNLSEQCKIGESVYKA
Sbjct 301 MYGTDAIMEATMNLSEQCKIGESVYKA 327
```

>dbj|BAG85154.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 667 bits (1720), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 324/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)

```
Query 5 FPFPLPHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVVTYIAQSPNFLSL 64
          FPFPLPHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVVTYIAQSPNFLSL
Sbjct 1 FPFPLPHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVVTYIAQSPNFLSL 60

Query 65 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 124
          TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF
Sbjct 61 TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSF 120

Query 125 YFVATTSYENLNTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 184
          YFVATTSYENLNTNWRVMDLNPVLSPNKLPIGIQV FPLFCKCPSKNQLDKEIKYLITYV
Sbjct 121 YFVATTSYENLNTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180

Query 185 WKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 244
          WKPGD+VSLVSDKFGASPEDIMSENNY QNFATAANNLPVLIPVTRLPVLARSPSDGRKGG
Sbjct 181 WKPGDDVSLVSDKFGASPEDIMSENNYDQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 240

Query 245 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKTlnrsassaetadkllsgvsgyvsKPT 304
          IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKTlnrsassaetadkllsgvsgyvsKPT
Sbjct 241 IRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKTlnrsassaetadkllsgvsgyvsKPT 300

Query 305 MYETDAIMEATMNLSEQCKIGESVYKA 331
          MYETDAIMEATMNLSEQCKIGESVYKA
Sbjct 301 MYETDAIMEATMNLSEQCKIGESVYKA 327
```

>dbj|BAG85169.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 665 bits (1717), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 324/327 (99%), Positives = 325/327 (99%), Gaps = 0/327 (0%)

```
Query 5 FPFPLPHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVVTYIAQSPNFLSL 64
          FPFPLPHSQILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSPSCETYVVTYIAQSPNFLSL
```

```

Sbjct 1      FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPSPSCETYVTYIAQSPNFLSL 60
Query 65      TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE 124
              TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE
Sbjct 61      TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE 120
Query 125     YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 184
              YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV
Sbjct 121     YFVATTSYENLTNRRVMDLNPVLSPNKLPIGIQVVFPLFCECPSKNQLDKEIKYLITYV 180
Query 185     WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 244
              WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG
Sbjct 181     WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 240
Query 245     IRLPVIIGISLGCTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 304
              IRLPVIIGISLGCTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVS YVSKPT
Sbjct 241     IRLPVIIGISLGCTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSRVYVSKPT 300
Query 305     MYETDAIMEATMNLSEQCKIGESVYKA 331
              MYETDAIMEATMNLSEQCKIGESVYKA
Sbjct 301     MYETDAIMEATMNLSEQCKIGESVYKA 327

```

>dbj|BAG85166.1| Nod factor receptor protein [Glycine max]
Length=327

Score = 660 bits (1702), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 322/324 (98%), Positives = 322/324 (98%), Gaps = 0/324 (0%)

```

Query 5      FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPSPSCETYVTYIAQSPNFLSL 64
              FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPSPSCETYVTYIAQSPNFLSL
Sbjct 1      FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPSPSCETYVTYIAQSPNFLSL 60
Query 65      TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE 124
              TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE
Sbjct 61      TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE 120
Query 125     YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 184
              YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEI+YLITYV
Sbjct 121     YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIRYLITYV 180
Query 185     WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 244
              WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG
Sbjct 181     WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 240
Query 245     IRLPVIIGISLGCTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 304
              IRLPVIIGISLGCTLLVLVLA VLLVYVYCLMKMTLNRSASSAE ADKLLSGVSGYVS+PT
Sbjct 241     IRLPVIIGISLGCTLLVLVLA VLLVYVYCLMKMTLNRSASSAENADKLLSGVSGYVSRPT 300
Query 305     MYETDAIMEATMNLSEQCKIGESV 328
              MYETDAIMEATMNLSEQCKIG SV
Sbjct 301     MYETDAIMEATMNLSEQCKIGISV 324

```



>dbj|BAG85147.1| Nod factor receptor protein [Glycine soja]
Length=327

Score = 659 bits (1700), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 320/327 (97%), Positives = 321/327 (98%), Gaps = 0/327 (0%)

```

Query 5      FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPSPSCETYVTYIAQSPNFLSL 64
              FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPSPSCETYVTYIAQSPNFLSL
Sbjct 1      FPFPLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFCSPSDSPSPSCETYVTYIAQSPNFLSL 60
Query 65      TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSE 124
              TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFAN SYEINQGDSE
Sbjct 61      TNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANTSYEINQGDSE 120
Query 125     YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 184
              YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV
Sbjct 121     YFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYV 180
Query 185     WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 244
              WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG
Sbjct 181     WKPGDNVSLVSDKFGASPEDIMSENNYQNFATAANNLPVLIPVTRLPVLARSPSDGRKGG 240
Query 245     IRLPVIIGISLGCTLLVLVLA VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 304
              IRLPVIIGI+LGCTLLVLVLA Y YCLMKMTLNRSASSAETADKLLSGVSGYVSKPT
Sbjct 241     IRLPVIIGIPLGCTLLVLVLA VLYAYWYGYCLMKMTLNRSASSAETADKLLSGVSGYVSKPT 300
Query 305     MYETDAIMEATMNLSEQCKIGESVYKA 331
              MYETDAIMEATMNLSEQCKIGESVYKA
Sbjct 301     MYETDAIMEATMNLSEQCKIGESVYKA 327

```

>ref|XP_002269472.1|  PREDICTED: hypothetical protein [Vitis vinifera]
emb|CB117584.3|  unnamed protein product [Vitis vinifera]
Length=590

GENE ID: 100259809 LOC100259809 | hypothetical protein LOC100259809
[Vitis vinifera] (10 or fewer PubMed links)

Score = 654 bits (1688), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 341/579 (58%), Positives = 424/579 (73%), Gaps = 7/579 (1%)

```

Query 23      STN-IVAQSQQDNRTNFCSPSDSPSPSCETYVTYIAQSPNFLSLTNISNIFDTSPLSIARA 81
              STN I AQS TNFSC +DSP SC+TYV Y AQ+P FL + NIS++F S LSIA A
Sbjct 16      STNHITAQSPATPVTFNFSCTTDSFASQTYVIYRAQAPGFLDVGNIISDLFGISRLSIAEA 75
Query 82      SNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSEYFVATTSYENLTNWRV 141
              SNL + +L DQ+LLVP+ C CTGN FANI+Y+I DSFYFV+ T +ENLTN+ AV
Sbjct 76      SNLASEEARLSPDQLLLVPILCSCTGNHYFANITYKIKTDDSFYFVSVTFENLTNYNAV 135
Query 142     MDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGAS 201
              LNP L P L +G++VVFPLFCKCPSK+ DK I YLITYVW+PGD+V LV AS
Sbjct 136     EALNPGLEPTTLQGVVVFPLFCKCPSKSHSDKGINYLITYVWQPGDDVLLVGTNLKAS 195

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Query 202 PEDIMSENNYGNFTAAANNLPVLIPVTRLPLVLARSPSDGRKGGIRLPVIIGISLGCTLLV 261
          P DI ENN NF+A+ + PVLIPV++ P+L + KG R + + +S G L+
Sbjct 196 PVDIRDENNN-NLNFSAVDQFVLIPVSPQPLLTQPERRASKG--RWILALVLSTGALLIF 252

Query 262 LVLAVLLVYVYCYLKMKTlnRSASSAETAD--KLLSGVSGYVSKPTMYETDAIMEATMNL 319
          L++++L+ K KTL+ S SS ET D KLL GVSgy+ KP MYET IMEATMNL+
Sbjct 253 LLVSLLVYTGLIRKKKTLdHSESSLETTDLIKLLPGVSGYLGKPIMYETKVMIEATMNLN 312

Query 320 EQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHNGLVKLMGVSSDNDGNCFFV 379
          E +IG SVY+A I G+V+AVK+ KED+TEEL+ILQKVNHNGLVKLMGVSSD DGN F+V
Sbjct 313 EHYRIGGSVYRATINGQVVAVKTKEDITEELRILQKVNHNGLVKLMGVSSDADGNRFLV 372



Query 380 YEYAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDI 439
          YE+AEENGSLD+WL K S +S+ A LTW QRI +A+DVA GLQYMHEH P +VHRDI
Sbjct 373 YEFAENGSLDKWLHPKPSSPSSSV-AFLTWSQRIQVALDVANGLQYMHEHTQPSVVHRDI 431

Query 440 TSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVLIELLTGRKAMTTKENGVEV 499
          ++NILLDS FKAKIANFSMA N MMPK+DVFAFGVVL+ELL+G+KAM + NGE+V
Sbjct 432 RANNILLDSRFKAKIANFSMATPAMNSMMPKVDFVFAFGVVLLELLSGKKAMQMRANGEIV 491

Query 500 MLWKDIWKIFDQENREERLKKWMDPKLESYYPIDYALSASLAVNCTADKSLSRPTIAE 559
          MLWKDI +I + E+ RE+R+++WMDP LE++YP D AL+LA LA +CT +KS +RP++AE
Sbjct 492 MLWKDIREILEVEDKREDRIRRWMDPTLENFYPFDGALNLAGLARSCTEQEKSSARPSMAE 551

Query 560 IVLSLSLLTQPSPATLERSLTSSGLDVEATQIVTISIAAR 598
          I +LS+L+Q S TLERS T E QI+ + AR
Sbjct 552 IAFNLSVLSQTSSETLERSWTQGFEPETIQTINPVIAR 590

```

>ref|XP_002533280.1|  serine-threonine protein kinase, plant-type, putative [Ricinus communis]
 gb|EEF29112.1|  serine-threonine protein kinase, plant-type, putative [Ricinus communis]
 Length=620

GENE ID: 8272992 RCOM 0411680 | serine-threonine protein kinase, plant-type, putative [Ricinus communis]

Score = 638 bits (1645), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 337/603 (55%), Positives = 427/603 (70%), Gaps = 32/603 (5%)

```

Query 23 STNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSLTNISNIFDTSPLSIARAS 82
          +T +AQ S Q TNFSC D P C+TYV Y AQ PNFL+L NIS++F S LSIA AS
Sbjct 23 TTYVTAGSPQG--TNFSCVDLPSPCQTYVAYYAQPNNFLNIGNISDLFAVSRLSIASAS 80

Query 83 NLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDsfYFVATTsYENLTNWRAVM 142
          NL D L+ +Q+LLVP+TCGCTGN SFANI+Y+I GDSFYFV+TT +ENL W+AV
Sbjct 81 NLVSEDPLMPNQQLLLVPITCGCTGNSSFANITYQIKPGDSFYFVSTTYFENLAKWQAVE 140

Query 143 DLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYVVKPGDNVSLVSDKFGASP 202
          NP L P L G +VVFPLECKCPSKNQ+ I+YLITYVW+P D++ V KF ASP
Sbjct 141 SFNPNLDPTLLHPGDKVVFPLFCKCPSKNQMKHGIQYLITYVWQPEDDIFKVGAKFNASP 200

Query 203 EDIMSENNYGNFTAAANNLPVLIPVTRLPLVLAR-SPSDGRKGGIRLPVIIGISLGCTLLV 261
          DI +NNY +F+ A + P+LIPVT++P+L++ SPS ++ L +II S+ LL+
Sbjct 201 HDIAIQNNYW-DFSTAVHHPLLIPVTQMPILSQSPSPSWPQRSEHHLVIIIVTSVAGALLI 259

Query 262 LVLAVLLVYVYCY----LKMKTlnRSASSAETA-----DKLLSGV 296
          +L LV+ +C K TL+R+ S ET DKLL GV
Sbjct 260 FLVAVFLVHAHCSCKKKKKTMTLHRNGSCLETTDLLQIKEQGKYSFEPKIIQDKLLPGV 319

Query 297 SGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQK 356
          SGY+ KP MY+ I+ ATM+L E +IG SVY+ANI G+VLAVK+ K D+TEEL ILQK
Sbjct 320 SGYLGKPIMYDIKEIILLATMDLHEHYRIGGSVYRANINGQVLAVKTKVDITEELNILQK 379

Query 357 VNHNGLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMA 416
          VNH NLVKLMG+SS+ DG+CF+VVEYAENGSLD+WL K + +S+S A L+W QR+ +A
Sbjct 380 VNHANLVKLMGISSNADGDCFLVVEYAENGSLDKWLHPKP-ASSSSSVAFLSWSQRLQIA 438



Query 417 VDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAF 476
          +DVA GLQYMHEH P +VH DI +SNILLDS FKAKIANFS+A+ T+ M+ K+DVFAF
Sbjct 439 LDVASGLQYMHEHIQPTVVHMDIRTSNILLDSRFKAKIANFSVAKLTDSMLQKVDVFAF 498

Query 477 GVVLIELLTGRKAMTTKENGVEVVMWKDIWKIFDQENREERLKKWMDPKLESYYPIDYA 536
          GVVL+ELL G+KAM T ENGE+V+LWK++ + + E R ERLLK MDP LE++YPID A
Sbjct 499 GVVILLELLCGKKAMVTNENGEIVLLWKEMKGVMEVAEKRAERLKKRMDPNLENFYPIDSA 558

Query 537 LSLASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATLERSLTSSGLDVEA-TQIVTISI 595
          LSLA+LA CT +KS +RP++AEIV +L++LTQ TLERS T SGL+ E QI + +
Sbjct 559 LSLANLARVCTLEKSSARPSMAEIVFNLTVTQSCSETLERSWT-SGLEAEEDIQTSPV 617

Query 596 AAR 598
          AR
Sbjct 618 IAR 620

```

>ref|XP_002310198.1|  predicted protein [Populus trichocarpa]
 gb|EEE90648.1|  predicted protein [Populus trichocarpa]
 Length=601

GENE ID: 7473142 POPTRDRAFT_870366 | hypothetical protein [Populus trichocarpa]
 (10 or fewer PubMed links)

Score = 614 bits (1583), Expect = 1e-173, Method: Compositional matrix adjust.
 Identities = 328/595 (55%), Positives = 423/595 (71%), Gaps = 17/595 (2%)

```

Query 14 ILCLVIMLFSTNIVAQSQQDNRTNFSCPSDSPSCETYVTYIAQSPNFLSLTNISNIFDT 73
          + LV++ FST + AQ+ TNFSCP DSP SC TY++Y+AQ P+FL L IS++F
Sbjct 14 LFFLVLVVFFSTYTYTAQAPPG--TNFSCPVDSPSTSCPTYISYLAQPPDFDLGKISHLFGI 71

Query 74 SPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDsfYFVATTsYE 133
          S IA ASNL D L +Q+LLVP+ CGCTG++SF NI+Y+I QGDS Y V+T S+E
Sbjct 72 SRTLIASASNLVSEDTPLEPNQQLLVPIRCGCTGSQSfVNITYQIQGDSIYSVSTISFE 131

Query 134 NLTNWRAVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYVVKPGDNVSL 193
          NLT W+ V LN L+P L G +V+PPLFCKCPS+ L+ I++LITYVW+PGD++

```

```

Sbjct 132 NLTRWQVEVEALNRSLTPTLLHAGDEVIFPLFCKCPSRTHLENGIEHLITYVWQPGDDLKK 191
Query 194 VSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVLAR---SPSDGRKGGIRL-PV 249
V+ AS +I+ ENNY NF AA P++IPV++LPVL++ +P R+G L V
Sbjct 192 VAAMLNASERNIENNY-DNFNAAVYNPIVIPVSKLPVLSQPYLTPE--RRGSKHLWIV 248
Query 250 IIGSLGCTLLVLVLAVLLVYVYC--LKMKTLNRSASSAETAD--KLLSGVSGYVSKPTM 305
I+ S+ T L L+ C K L+R+ S ET+D KLL GV G + K +
Sbjct 249 IVAASIASTFTTCPLVAFLIHKRCSYKATKALDRGTGSCLETSDPKLLPGVLGCLDKSII 308
Query 306 YETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRKEDVTEELKILQKVNHGNNLVKL 365
YE AIME TM+L E KIG SVY+ANI G VLAVK+ K+DVTEELKILQKV+H NLVKL
Sbjct 309 YEVKAIMEGTMDLHEHYKIGGSVYRANINGCVLAVKKTKDDVTEELKILQKVSHANLVKL 368
Query 366 MGVSDDND--GNCFFVVEYAENGSLDEWLFSSKSCSDTSNSRASLTWCQRISMAVDVAMGL 423
MG+SS++D GN F+VVEYAENGSLD+WL KS +S+S LTW QR+ +A+DVA GL
Sbjct 369 MGMSSSDREGRNFLVVEYAENGSLDKWLHPKS-ESSSSSVGFLLTWKQRMQVALDVANGL 427
Query 424 QYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMMPKIDVFAFGVVLIEL 483
QY+HEH PR VH+DI +SNILLDS F+AKIANFSMAR T+ MMPK DVF FGVVL+EL
Sbjct 428 QYLHEHQPRTVHKDIRTSNILLDSTFRAKIANFSMARAATDSMMPKDDVDFGVVLLEL 487
Query 484 LTGRKAMTTKENGEEVVMWLKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYALSASLA 543
L+G+KAM TKE GE+V+L ++I + + EE REERL+KWM DP LE +YPD A+SLA+LA
Sbjct 488 LSGKKAMVTKEKGEIVLLCREIKDVLEMEEKREERLKKWMDPNLERFYPIDSAMS LATLA 547
Query 544 VNCTADKSLSRPTIAEIVLSLSLLTQSPATLERSLTSSGLDVEATQIVTSIAAR 598
CT +KS RP++AEIV +L+LTQ SP TLER TS + T+V+ + AR
Sbjct 548 RLCTLEKSSSERPMAEIVFNLTVLTLQSSPETLER-WTSEVETEDFTRLVSPVTAR 601

```

>emb|CA002936.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=349

Score = 499 bits (1285), Expect = 4e-139, Method: Compositional matrix adjust.
Identities = 248/351 (70%), Positives = 290/351 (82%), Gaps = 4/351 (1%)

```

Query 54 YIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFAN 113
Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLVPVTCGCT N SFAN
Sbjct 1 YRAQSPNFLSLSNISDIFNLSPLRIAKASNIEAEDKKLIPDQLLLVPVTCGCTKNHSFAN 60
Query 114 ISYEINQGDSEFYFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQL 173
I+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCKCPSKNQL
Sbjct 61 ITYSIKQGDNEFILLSITSYQNLNTNLEFKNFNPNSPTLLPLDTKVSVPLFCKCPSKNQL 120
Query 174 DKEIKYLITYVWVKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVTRLPVL 233
+K IKYLITYVW+ DNV+LVS KFGAS ++++ENN+ NFTA+ N VLIPVT LP L
Sbjct 121 NKGIKYLITYVWQDNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPVTSLPKL 178
Query 234 ARSPSDGRKGGIR-LPVIIGISLGCTLLVLVLAVLLVYVYCLKMKTLNRSASSAETADKL 292
+ S+GRK + L +IIGISLG +LVL + LVYVYCLKMK LNRS SS+ETADKL
Sbjct 179 DQPSNNGRKKSSSQNLALIIGISLGAFFILVLTLSLVYVYCLKMKRLNRSSTSSSETADKL 238
Query 293 LSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRKEDVTEELK 352
LSGVSGVSKPTMYE DAIME TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
Sbjct 239 LSGVSGVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK 298
Query 353 ILQKVNHGNNLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSSKSCSDTSNS 403
ILQKVNHGNNLVKLMGVSSDNDGNCFFVVEYAENGSL+EWLFS+S S TSNS
Sbjct 299 ILQKVNHGNNLVKLMGVSSDNDGNCFLVVEYAENGSLDEWLFSES-SKTSNS 348

```

>emb|CA002948.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=337

Score = 484 bits (1245), Expect = 2e-134, Method: Compositional matrix adjust.
Identities = 238/339 (70%), Positives = 278/339 (82%), Gaps = 3/339 (0%)

```

Query 49 ETYYTYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGN 108
ETVY Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLVPVTCGCT N
Sbjct 1 ETYVAYRAQSPNFLSLSNISDIFNLSPLRIAKASNIEAEDKKLIPDQLLLVPVTCGCTKN 60
Query 109 RSFANISYEINQGDSEFYFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVPFLFCKCP 168
SFANI+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCKCP
Sbjct 61 HSFANIYYSIKQGDNEFILLSITSYQNLNTNLEFKNFNPNSPTLLPLDTKVSVPLFCKCP 120
Query 169 SKNQLDKEIKYLITYVWVKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLPVLIPVT 228
SKNQL+K IKYLITYVW+ DNV+LVS KFGAS ++++ENN+ NFTA+ N VLIPVT
Sbjct 121 SKNQLNKGIKYLITYVWQDNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPVT 178
Query 229 RLPVLARSPPSDGRKGGIR-LPVIIGISLGCTLLVLVLAVLLVYVYCLKMKTLNRSASSAE 287
LP L+ S+GRK + L +IIGISLG +LVL + LVYVYCLKMK LNRS SS+E
Sbjct 179 SLPKLDQPSNNGRKKSSSQNLALIIGISLGAFFILVLTLSLVYVYCLKMKRLNRSSTSSSE 238
Query 288 TADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRKEDV 347
TADKLLSGVSGYVSKPTMYE DAIME T NLS+ CKIGESVYKANI+G+VLAVK+ K+D
Sbjct 239 TADKLLSGVSGYVSKPTMYEIDAIMEGTNLSNCKIGESVYKANIDGRVLAVKKIKKDA 298
Query 348 TEELKILQKVNHGNNLVKLMGVSSDNDGNCFFVVEYAENG 386
+EELKILQKVNHGNNLVKLMGVSSDNDGNCFFVVEYAENG
Sbjct 299 SEELKILQKVNHGNNLVKLMGVSSDNDGNCFLVVEYAENG 337

```

>emb|CA002942.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=334

Score = 481 bits (1238), Expect = 1e-133, Method: Compositional matrix adjust.
Identities = 237/336 (70%), Positives = 277/336 (82%), Gaps = 3/336 (0%)

```

Query 54 YIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFAN 113
Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLVPVTCGCT N SFAN
Sbjct 1 YRAQSPNFLSLSNISDIFNLSPLRIAKASNIEAEDKKLIPDQLLLVPVTCGCTKNHSFAN 60
Query 114 ISYEINQGDSEFYFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQL 173
I+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCKCPSKNQL

```

```

Sbjct 61 ITYSIKQGDNFFILSITSYQNLNTYLEFKNFNPNLSPDLLPLDTKVSVPFLFCKCPSKNQL 120
Query 174 DKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPTVTRLPVL 233
+K IKYLIITYVW+ DNV+LVS KFGAS +++ENN+ NFTA+ N VLIPVT LP L
Sbjct 121 NKGIKYLITYVWQDNNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPTVTSLPKL 178
Query 234 ARSPSDGRKGIR-LPVIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKL 292
+ S+GRK + L +IIGISLG +LVL + LVYVYCLMK LNRS SS+ETADKL
Sbjct 179 DQPSNGRKGSSQNLAIIIGISLGAFFILVLTLSLVYVYCLMKRLNRSTSSSETADKL 238
Query 293 LSGVSGVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 352
LSGVSGVSKPTMYE DAIME TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
Sbjct 239 LSGVSGVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK 298
Query 353 ILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSL 388
ILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSL
Sbjct 299 ILQKVNHNGLVKLMGVSSDNDGNCFLVVEYAENGSL 334

```



>emb|CA002960.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=333

Score = 477 bits (1228), Expect = 2e-132, Method: Compositional matrix adjust.
Identities = 235/335 (70%), Positives = 275/335 (82%), Gaps = 3/335 (0%)

```

Query 54 YIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFAN 113
Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLVPVTCGCT N SFAN
Sbjct 1 YRAQSPNFLSLSNISDIFNLSPLRIAKASNIEAEDKKLIPDQLLLVPVTCGCTKNHSFAN 60
Query 114 ISYEINQGDSEFYFVATTSYENLNTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQL 173
I+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCKCPSKNQL
Sbjct 61 ITYSIKQGDNFFILSITSYQNLNTYLEFKNFNPNLSPDLLPLDTKVSVPFLFCKCPSKNQL 120
Query 174 DKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPTVTRLPVL 233
+K IKYLIITYVW+ DNV+LVS KFGAS +++ENN+ NFTA+ N VLIPVT LP L
Sbjct 121 NKGIKYLITYVWQDNNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPTVTSLPKL 178
Query 234 ARSPSDGRKGIR-LPVIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKL 292
+ S+GRK + L +IIGISLG +LVL + LVYVYCLMK LNRS SS+ETADKL
Sbjct 179 DQPSNGRKGSSQNLAIIIGISLGAFFILVLTLSLVYVYCLMKRLNRSTSSSETADKL 238
Query 293 LSGVSGVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 352
LSGVSGVSKPTMYE DAIME T NLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
Sbjct 239 LSGVSGVSKPTMYEIDAIMEGTTNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK 298
Query 353 ILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSL 387
ILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSL
Sbjct 299 ILQKVNHNGLVKLMGVSSDNDGNCFLVVEYAENGSL 333

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>ref|XP_002468236.1|  hypothetical protein SORBIDRAFT_01g042230 [Sorghum bicolor]
gb|EER95234.1|  hypothetical protein SORBIDRAFT_01g042230 [Sorghum bicolor]
Length=631

GENE ID: 8085264 SORBIDRAFT_01g042230 | hypothetical protein [Sorghum bicolor]
(10 or fewer PubMed links)

Score = 441 bits (1133), Expect = 2e-121, Method: Compositional matrix adjust.
Identities = 256/589 (43%), Positives = 352/589 (59%), Gaps = 57/589 (9%)

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Query 32 QDNRTNFSCP-----SDSPPSCEYVYIAQSPNFLSLTNISNIFDTSPLSIARASN 84
QDN TN++ P S SPP C+TYV Y QSP + L +IS++F TS IA A+ L
Sbjct 22 QDN-TNYTVPAQFACNVSSPPPCDTYVVYRTQSPGYDGLGSIISDLFGTSQARTASANGL 80
Query 85 EPMDDKLVKDQVLLVPVT-CGCTGNRSFANISYEINQGDSEFYFVATTSYENLNTNWRVMD 143
D L Q LLVPV+ CGCTG SFAN++Y I QGD+F+ +A SYENLT ++ + +
Sbjct 81 SSEDGVLQPQPLLVLPVSKCGCTGGWSFANVTYPIRQGDFTFFNLARVSYENLTYQLIQ 140
Query 144 LNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPE 203
LNP P L +G +V PLFC+CP+ E ITYVW+ GD +S VS + +
Sbjct 141 LNP RSVPTSLVGQEVTVPLFCRC PAP----AERSSFITVYWQAGDTMSQVSKLMNTTED 196
Query 204 DIMSENNYQGNFTAAN--NLPVLIPTVTRLPVL-----ARSPSDGRKGIRLPVIIGISLG 256
+I NN + +A+ P+LIPV + P L A S DG+ R VIIG S+
Sbjct 197 EIAEANNVTSSSASASLVGQPM LIPVQQRPLPLHYAASAGDGKSRWRRRAVIIGASVS 256
Query 257 CTLLVLVLAVLLVYVYCLK-----MKT LNRSASSAE----- 287
+ V+ LA L V + L+ M+ +R A + +
Sbjct 257 GS--VVALAALFVAILALRRYRKPKSMRLGSRFAVNTKLTWSRNQFGHDSNSNFAHMMKL 314
Query 288 TADKLLSGVSGVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDV 347
KLL+GVS ++ KP ++ + IMEATMNL E+CKIG + Y+A ++G+V AVK K DV
Sbjct 315 KGGKLLTGVSFEFDKPIIFLEEBIMEATMNLDERCKIGSTYYRAKLDGEVFAVKPAKGDV 374
Query 348 TEELKILQKVNHNGLVKLMGVSSDNDGN-CFVVVEYAENGSLDEWLFESKSCSDTSNSR-- 404
+ ELK++Q VNH NL+KL G+S DG+ F+VE+AE GSLD+WL+ K S +S
Sbjct 375 SAELKMMQMNVNHNLIKLAGISIGTDGDYAFVLYEFAEKGS LDKWLYQKPPSALPSSSCC 434
Query 405 --ASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFMSMAR- 461
A+L+W QR+S+A+DVA GL YMHEH P +VH DI + NILL + F+ KI+ FS+A+
Sbjct 435 TVATLSWGQRLSIALDVANGLLYMHEHTQPSMVHGDIRARNILLTAEFRTKISGFS LAKP 494
Query 462 TFTNPMMPKIDVFAFGVVLIELLTGRKAMTTKENGVEVVMWLKDIWKIFDQENREERLKK 521
+ DVFAFG++L+ELL+GR+AM + E+ MLW+I + D + RE +L K
Sbjct 495 ATADAAATSSDVFAFGLLLELLSGRRAMEARVGSEIGMLWREIRGVLDAGDKREAKLGK 554
Query 522 WMDPKLESYYPIDYALSASLAVNCTADKLSRPTIAEIVLSLSLLTQP 570
WMDP L S Y +D ALSLA +A CT D + RP + E+V SLS+L QP
Sbjct 555 WMDPALGSEYHMDAALS LAGMARCTEDDAARRPNMTEVVFSLSVLVQP 603

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>emb|CA002953.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=313

Score = 436 bits (1120), Expect = 6e-120, Method: Compositional matrix adjust.

Identities = 216/315 (68%), Positives = 255/315 (80%), Gaps = 3/315 (0%)

Query	54	YIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFAN	113
Sbjct	1	Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLVPVTCGCT N SFAN	60
Query	114	ISYEINGQDSFYFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQL	173
Sbjct	61	ITYSIKQGDNFFILSITSYQNLTNYLEFKNFNPNSPTLLPLDTKVSVPLFCKCPSKNQL	120
Query	174	DKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYGQNF TAANNLPVLIPVTRLPVL	233
Sbjct	121	+K IKYLITYVW+ DNV+LVS KFGAS ++++ENN+ NFTA+ N VLIPVT LP L	178
Query	234	ARSPSDGRKGGR-LPVIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKL	292
Sbjct	179	+ S+GRK + L +IIGISLG +LVL + LVYVYCLMKM LNRS SS+ETADKL	238
Query	293	LSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK	352
Sbjct	239	LSGVSGYVSKPTMYE DAIME T NLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK	298
Query	353	ILQKVNHNGLVKLMG 367	
Sbjct	299	ILQKVNHNGLVKLMG 313	

>emb|CA002964.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
 >emb|CA002968.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
 Length=311

Score = 433 bits (1113), Expect = 4e-119, Method: Compositional matrix adjust.
 Identities = 215/313 (68%), Positives = 254/313 (81%), Gaps = 3/313 (0%)

Query	54	YIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFAN	113
Sbjct	1	Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLVPVTCGCT N SFAN	60
Query	114	ISYEINGQDSFYFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQL	173
Sbjct	61	ITYSIKQGDNFFILSITSYQNLTNYLEFKNFNPNSPTLLPLDTKVSVPLFCKCPSKNQL	120
Query	174	DKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYGQNF TAANNLPVLIPVTRLPVL	233
Sbjct	121	+K IKYLITYVW+ DNV+LVS KFGAS ++++ENN+ NFTA+ N VLIPVT LP L	178
Query	234	ARSPSDGRKGGR-LPVIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKL	292
Sbjct	179	+ S+GRK + L +IIGISLG +LVL + LVYVYCLMKM LNRS SS+ETADKL	238
Query	293	LSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK	352
Sbjct	239	LSGVSGYVSKPTMYE DAIME TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK	298
Query	353	ILQKVNHNGLVKL 365	
Sbjct	299	ILQKVNHNGLVKL 311	

>emb|CA002944.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
 Length=307

Score = 427 bits (1097), Expect = 2e-117, Method: Compositional matrix adjust.
 Identities = 211/309 (68%), Positives = 250/309 (80%), Gaps = 3/309 (0%)

Query	54	YIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFAN	113
Sbjct	1	Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLVPVTCGCT N SFAN	60
Query	114	ISYEINGQDSFYFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQL	173
Sbjct	61	ITYSIKQGDNFFILSITSYQNLTNYLEFKNFNPNSPTLLPLDTKVSVPLFCKCPSKNQL	120
Query	174	DKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYGQNF TAANNLPVLIPVTRLPVL	233
Sbjct	121	+K IKYLITYVW+ DNV+LVS KFGAS ++++ENN+ NFTA+ N VLIPVT LP L	178
Query	234	ARSPSDGRKGGR-LPVIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKL	292
Sbjct	179	+ S+GRK + L +IIGISLG +LVL + LVYVYCLMKM LNRS SS+ETADKL	238
Query	293	LSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK	352
Sbjct	239	LSGVSGYVSKPTMYE DAIME TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK	298
Query	353	ILQKVNHN 361	
Sbjct	299	ILQKVNHN 307	

>gb|AAM19130.1|AC103891.10 Putative protein kinase [Oryza sativa Japonica Group]
 >gb|ABF94815.1| Protein kinase domain containing protein [Oryza sativa (japonica cultivar-group)]
 >gb|EAZ26175.1| hypothetical protein OsJ_10042 [Oryza sativa Japonica Group]
 Length=624

Score = 426 bits (1096), Expect = 3e-117, Method: Compositional matrix adjust.
 Identities = 251/600 (41%), Positives = 355/600 (59%), Gaps = 43/600 (7%)

Query	10	LHSQILCLVIMLFSTNVAQSQQDNRT----NFSCPSDSPSPSCETYTYIAQSPNFLSLT	65
Sbjct	1	+ + LC++ ++ + + + T F+C +P C+T+V Y QSP FL L	58
Query	66	MEHGKLCILAVVIAFQLAGGEAVTDATARARRFACNVSA--CDTFVVYRTQSPGFLDLG	
Query	66	NISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINGQDSFY	125
		NIS++F S IA A+ L D L+ Q LLVPV CGCTG RSFAN++Y I D+F+	

Sbjct	59	NISDLFGVSRALIASANKLTEDGVLLPGQPLLVPVKCGCTGARSFANVTYPIRPRDTFF	118
Query	126	FVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCCKPSKNQLDKEIKYLITYVW +A T++ENLT++ V +LNP +L +VV PLFC+CP++ +L +L+TYVW	185
Sbjct	119	GLAVTAFENLTDVFLVEELNPAEATRLEPWQEVVVPLFCRCPTREELSAGSRLLVITYVW	178
Query	186	KPGDNVSLVSDKFGASPEDIMSENNYGQNF TAANNLPVLIPVTRLP-----VLARSP +PGD+VS+VS AS +I + N N T A PVLIPV++ P +A P	237
Sbjct	179	QPGDDVSVVSALMNASANAASNGVAGNSTFATGQPVLI PVSQPPRFPPLTYGAIADP	238
Query	238	SDG--RKGGIRLPVIGISLGCTLLVLVLAVLLVYVYCLKM-----KTLNRS G R G I I G + C VL A+L Y K K+LNR	282
Sbjct	239	GAGKHRHGII VATS IAGSFVACA--VLCTAILAYRRYRKAPVPHVSPKLSWTKSLNRF	296
Query	283	ASSAETA-----DKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGK S++ A DKLL+ VS ++ KP ++ + IMEATMNL EQCK+G S Y+AN+E +	336
Sbjct	297	DSNSSIARMINGGDKLLTSVSQFIDKPIIFREEEIMEATMNLDEQCKLGSSYYRANLERE	356
Query	337	VLA VKR FKEDVTEELKILQKVNHG NLVKLMGVSSDNDGN-CFVVY EYAENGSLDEWLFSK V AVK K +V EL+++Q VNH NL KL G+S DG+ F+VYE+AE GS LD+WL+ K	395
Sbjct	357	VFAVKPAKGNVAGELRMMQMVNHANLTKLAGISIGADGDYAF LVYEF AEKGS LDKWLYQK	416
Query	396	SCSDTSNSR--ASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAK +S A+L+W QR+ +A+DVA GL Y+HEH P +VH D+ + NILL + F+AK	453
Sbjct	417	PPCSQPSSSSVATLSWDQRLGIALDVANGLLYLHEHTQPSMVHGDVRARNILLTAGFRAK	476
Query	454	IANFSMAR--TFTNPMMPKIDVFAFGVVLIELLTGRKAMTTKENG EVVMLWKDIWKIFDQ ++NFS+A+ + DVFAFG++L+ELL+GR+A+ + E+ ML +I + D	511
Sbjct	477	LSNFS LAKPAAMVDAATSSDVFAFGLLLELLSGRAVEARVGVEIGMLRTEIRTVLDA	536
Query	512	-EENREERLKKWMDPKLESYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSLSLLTQP + R +L+KWM DP L Y +D ALSLA +A CT + + RP +AEI SLS+L QP	570
Sbjct	537	GGDKRAAKLRKWM DPTLGGEYGVDAALSLAGMARACTEEDAARRPKMAEIAFSLSVLGQP	596

>gb|EAY89155.1| hypothetical protein OsI_10648 [Oryza sativa Indica Group]
Length=624

Score = 426 bits (1094), Expect = 6e-117, Method: Compositional matrix adjust.
Identities = 251/600 (41%), Positives = 355/600 (59%), Gaps = 43/600 (7%)

Query	10	LHSQILCLVIMLFSTNIVAQSQQDNRT---NFSCPSDSPSCETYVITYAQSPNFLSLT + + LC++ ++ + + + T F+C +P C+T+V Y QSP FL L	65
Sbjct	1	MEHKGLCILAVVIAFQLAGGQAVTDATARARRFACNV SAP--CDTFVYVRTQSPGFLDLG	58
Query	66	NISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSFY NIS++F S IA A+ L D L+ Q LLVPV CGCTG RSFAN++Y I D+F+	125
Sbjct	59	NISDLFGVSRALIASANKLTEDGVLLPGQPLLVPVKCGCTGARSFANVTYPIRPRDTFF	118
Query	126	FVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCCKPSKNQLDKEIKYLITYVW +A T++ENLT++ V +LNP +L +VV PLFC+CP++ +L +L+TYVW	185
Sbjct	119	GLAVTAFENLTDVFLVEELNPAEATRLEPWQEVVVPLFCRCPTREELSAGSRLLVITYVW	178
Query	186	KPGDNVSLVSDKFGASPEDIMSENNYGQNF TAANNLPVLIPVTRLP-----VLARSP +PGD+VS+VS AS +I + N N T A PVLIPV++ P +A P	237
Sbjct	179	QPGDDVSVVSALMNASANAASNGVAGNSTFATGQPVLI PVSQPPRFPPLTYGAIADP	238
Query	238	SDG--RKGGIRLPVIGISLGCTLLVLVLAVLLVYVYCLKM-----KTLNRS G R G I I G + C VL A+L Y K K+LNR	282
Sbjct	239	GAGKHRHGII VATS IAGSFVACA--VLCTAILAYRRYRKAPVPHVSPKLSWTKSLNRF	296
Query	283	ASSAETA-----DKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGK S++ A DKLL+ VS ++ KP ++ + IMEATMNL EQCK+G S Y+AN+E +	336
Sbjct	297	DSNSSIARMINGGDKLLTSVSQFIDKPIIFREEEIMEATMNLDEQCKLGSSYYRANLERE	356
Query	337	VLA VKR FKEDVTEELKILQKVNHG NLVKLMGVSSDNDGN-CFVVY EYAENGSLDEWLFSK V AVK K +V EL+++Q VNH NL KL G+S DG+ F+VYE+AE GS LD+WL+ K	395
Sbjct	357	VFAVKPAKGNVAGELRMMQMVNHANLTKLAGISIGADGDYAF LVYEF AEKGS LDKWLYQK	416
Query	396	SCSDTSNSR--ASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAK +S A+L+W QR+ +A+DVA GL Y+HEH P +VH D+ + NILL + F+AK	453
Sbjct	417	PPCSQPSSSSVATLSWDQRLGIALDVANGLLYLHEHTQPSMVHGDVRARNILLTAGFRAK	476
Query	454	IANFSMAR--TFTNPMMPKIDVFAFGVVLIELLTGRKAMTTKENG EVVMLWKDIWKIFDQ ++NFS+A+ + DVFAFG++L+ELL+GR+A+ + E+ ML +I + D	511
Sbjct	477	LSNFS LAKPAATVDAATSSDVFAFGLLLELLSGRAVEARVGVEIGMLRTEIRTVLDA	536
Query	512	-EENREERLKKWMDPKLESYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSLSLLTQP + R +L+KWM DP L Y +D ALSLA +A CT + + RP +AEI SLS+L QP	570
Sbjct	537	GGDKRAAKLRKWM DPTLGGEYGVDAALSLAGMARACTEEDAARRPKMAEIAFSLSVLGQP	596

>emb|CA002946.1| LysM-domain containing receptor-like kinase [Medicago truncatula
var. truncatula]
Length=305

Score = 422 bits (1085), Expect = 6e-116, Method: Compositional matrix adjust.
Identities = 209/307 (68%), Positives = 248/307 (80%), Gaps = 3/307 (0%)

Query	54	YIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFAN Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLVPVTCGCT N SFAN	113
Sbjct	1	YRAQSPNFLSLSNISDIFNLSP LRIAKASNIEAEDKKLIPDQLLLVPVTCGCTKNHSFAN	60
Query	114	ISYEINQGDSFYFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCCKPSKNQL I+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCCKPSKNQL	173
Sbjct	61	ITYSIKQGDNFILSITSYQNLNTYLEFKNFENPNLSPTLLPLD TKVSVPLFCCKPSKNQL	120
Query	174	DKEIKYLITYVWVKPGDNVSLVSDKFGASPEDIMSENNYGQNF TAANNLPVLIPVTRLPV +K IKYLITYVW+ DNV+LVS KFGAS +++ENN+ NFTA+ N VLIPVT LP L	233
Sbjct	121	NKGIKYLITYVWQDNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPVTSLEPKL	178
Query	234	ARSPSDGRKGGR-LPVIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKL + S+GRK + L +IIGISLG +LVL +LVYVYCLMK LNRS SS+ETADKL	292
Sbjct	179	DQPSNGRKGSSQNLALIIGISLGS AFFILVLTLSLVYVYCLMKRLNRSSTSETADKL	238
Query	293	LSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKR FKEDVTEELK LSGVSGYVSKPTMYE DAIME TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK	352
Sbjct	239	LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDASEELK	298

Query 353 ILQKVN 359
ILQKVN
Sbjct 299 ILQKVN 305

>emb|CA002962.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=304

Score = 418 bits (1075), Expect = 9e-115, Method: Compositional matrix adjust.
Identities = 208/306 (67%), Positives = 247/306 (80%), Gaps = 3/306 (0%)

Query 54 YIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFAN 113
Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLVPVTCGCT N SFAN
Sbjct 1 YRAQSPNFLSLSNISDIFNLSPLRIAKASNIEADKKLIPDQLLLVPTVTCGCTKNHSFAN 60

Query 114 ISYEINQGSDFYFVATTSYENLTNWRVMDLNPVLSFNKLPVIGIQVVFPLFCCKCPSKNQL 173
I+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCCKCPSKNQL
Sbjct 61 ITYSIKQGDNFFILSITSYQNLNTNYLEFKNFNPNLSPTLLPLDTKVSVPFLFCCKCPSKNQL 120


Query 174 DKEIKYLITYVVKPGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLPVLIPTVTRLPVL 233
+K IKYLITYVW+ DNV+LVS KFGAS +++ENN+ NFTA+ N VLIPVT LP L
Sbjct 121 NKGKIKYLITYVWQNDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPVTSPLPKL 178

Query 234 ARSPSDGRKGIR-LPVIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKL 292
+ S+GRK + L +IIGISLG +LVL + LVYVYCLMK LNRS SS+ETADKL
Sbjct 179 DQPSSNGRKSSSQNLALIIGISLGSAFFILVLTLSLVYVYCLMKRNLNRSTSSSETADKL 238

Query 293 LSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 352
LSGVSGYVSKPTMYE DAIME TMNLS+ CKIGESVYKANI+G+VLAVK+ K+D +EELK
Sbjct 239 LSGVSGYVSKPTMYEIDAIMEGTMNLSDNCKIGESVYKANIDGRVLAVKKIKKDAEELK 298

Query 353 ILQKVN 358
ILQKVN
Sbjct 299 ILQKVN 304

>ref|XP_002517029.1|  serine-threonine protein kinase, plant-type, putative [Ricinus communis]

gb|EEF45192.1|  serine-threonine protein kinase, plant-type, putative [Ricinus communis]
Length=615

GENE ID: 8280185 RCOM_0909430 | serine-threonine protein kinase, plant-type, putative [Ricinus communis]

Score = 366 bits (939), Expect = 5e-99, Method: Compositional matrix adjust.
Identities = 216/566 (38%), Positives = 324/566 (57%), Gaps = 65/566 (11%)

Query 48 CETYVTYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGC-- 105
C+TY Y A +PNFL L ++ +F S L I+ SN+ L+ +Q L VP++C C
Sbjct 44 CQTYAFYRAMAPNFDLDASVGDLSFVSRLMISEPSNISSPSSPLIPNQSLFVPISSCRA 103

Query 106 ---TGNRSFANISYEINQGSDFYFVATTSYENLTNWRVMDLNPVLSFNKLPVIGIQVVF 162
T N S+AN+SY I + D+FY V+TT ++NLT ++AV +NP L P L IG +V+FP
Sbjct 104 INSTNLSYANLSYTIKKDDTFYLVSTTQFQNLTTYQAVQVNPVTLVPTLLEIGQEVIFP 163

Query 163 LFCKCPKQDLKDKIKYLITYVVKPGDNVSLVSDKFGASPEDIMSENNYQGNFTAANNLP 222
+FCKCP++ QL ++ ++I+YV++P DN+SLV+ FG + + I+ N G N +
Sbjct 164 VFCKCPNQTLQNLQVNFMSYVFPQPSDNLSLVASSFGTNTQSIQVDVN--GNNIQPFDT-- 219

Query 223 VLIPVTRLPVLARS---PSDGRKGIRLPVIGISLGCTLLVLVLAVLLVYVYCLMKMTL 279
+ +PV RLP L++ PS + R +I G+++G + +L +L++ + + L
Sbjct 220 IFVFNRLPLQSPQVVPVSPVTEKKERKGLITGLAVGLGVCGLL-ILIIGSVWFREGKL 278

Query 280 NRSASS-----AETADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQC 322
NR S E KL++ VS + K +++ D + EAT +E
Sbjct 279 NRKSEEDDKRLRFYKGEKGLTEMETKLIADVSDCLDKYRVFKIDELKEATDGFENEF 338


Query 323 KIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGKLVKMGVSSDN-DGNCFFVYE 381
I SVYK +I G+ A+K+ K + EELKILQKVNHGKLVKL G D+ DG+C+++YE
Sbjct 339 LIQGSVYKGSINGQDYAIKKMKWNAYEELKILQKVNHGKLVKLEGFCIDSEDDGSCYLIYE 398

Query 382 YAENGSLDEWLFKSKSDTNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITS 441
Y ENGS L WL N L W R+ +A+DVA GLQY+HEH PR+VH+DI S
Sbjct 399 YIENGSLHSLWLH-----INKNEKLNWKTRRLRIAIDVANGLYIHEHTRPRVVKDIKS 451

Query 442 SNILLDSNFRAKIANFSMARTFTNPM-----PKIDVFAFGVVL 480
SNILLDS +AKIANF +A++ N + ++DVE+FGVVL
Sbjct 452 SNILLDSTMRAKIANFGLAKSGCNAITMHIVGTQGYIAPEYLTGCVSTRMDFVSGVVL 511

Query 481 IELLTGRKAMTTKENGSEVVMWLKDIWKIFD-QUEENREERLKKWMDPK-LESYPIDYALS 538
+EL++G++A+ E G V LW + +D EE + +RLK +MD L ++ +
Sbjct 512 LELISGKEAT--DEEGRV--LWAKVSGNWDGNEKKVKRLKGFMDSESLRESMSMESIIH 567

Query 539 LASLAVNCTADKSLSRPTIAEIVLSL 564
+ ++AV C RP++ +IV L
Sbjct 568 VMNVAVACLHKDPKRPSMVDIVYL 593

>ref|XP_002280070.1|  PREDICTED: hypothetical protein [Vitis vinifera]
Length=622

GENE ID: 100264758 LOC100264758 | hypothetical protein LOC100264758 [Vitis vinifera]

Score = 355 bits (912), Expect = 8e-96, Method: Compositional matrix adjust.
Identities = 220/589 (37%), Positives = 329/589 (55%), Gaps = 68/589 (11%)

Query 28 AQSQ-QDNRTNFSCPSD-SPPSCETYVTYIAQSPNFLSLTNISNIFDTSPLSIARASNLE 85
+Q+Q +N T + C ++ S C T+ Y A SPNFL L +I ++F S L I+ SN+
Sbjct 27 SQAQPEPNATGYPCSANLSSYPCHTFAYTATSPNFLDLASIGDLFWVSRMISEPSNIS 86

Query 86 PMDDKLVKDQVLLVPVTCGC-----TGNRSFANISYEINQGSDFYFVATTSYENLTNWR 140
+ LV Q L VP+ C C T S+AN+SY I GD+FY V+T S+ NLT + +

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Sbjct 87 SPSNPLVAGQSLFVPLNCSCNSVNTTTAISYANLSYTIKSGDTFYLVSTFSFLNLTYYYS 146
Query 141 VMDLNPVLSPNPKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGA 200
V +NP L P L +G +V+FP+FCCKCP++ QL + +LI+YV++P DN++ V+ G+
Sbjct 147 VEIVNPFLVPTDLDVGDKVIFPIFCCKPNETQLRNGVNFLLISYVFPQSDNLTGVAASLGS 206
Query 201 SPEDIMSENNGQNTAANNLPVLIPVTRLP-----VLARSPSDGRKGGIRLPVIIGIS 254
I+ N G N + +PV+RLP V A + RK R VIIG++
Sbjct 207 DTASIIDVN--GDNIQPFQT--IFVPVSRLENISQPNVTASVATSVRKVE--RKGVIIGLA 261
Query 255 LG---CTLLVLVLAVLLVYVYCL--KMKTLL-----NRSASSAETADKLLSGVSGYV 300
+G C +L+++L + VY + + K+K + R L++ VS +
Sbjct 262 IGLGVCIGILLVLLIGVWVYRHVMVEKIKEIEGDKERPLVGRGTGLKAEENVLMADVSDCL 321
Query 301 SKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHG 360
K +Y + + +AT SE+ I SVYK +I+G++ A+K+ K + EELKILQKVNHG
Sbjct 322 DKYKVYGIEELRDATGGFSERSLIQGSVYKGSIDGELYAIKKMKWNAYEELKILQKVNHG 381
Query 361 NLVKLMGVSSD--NDGNCFFVVEYAENGSLDEWLFKSCSDTSNSRASLTWCQRISMAVDV 419
NLV+L G D D C++VE+ ENGL WL + L W R+ +A+DV
Sbjct 382 NLVRLEGFCIDPEDATCYLVYEFVENGSLQSWLH-----GDRDEKLNWKNRLRIAIDV 434
Query 420 AMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPM----- 468
A GLQY+HEH PR+VH+DI SSNILL N +AKIANF +A++ N +
Sbjct 435 ANGLQYIHEHTRPRVHKDIKSSNILLDGNMRAKIANFGLAKSGCNAITMHIVGTQGYIA 494
Query 469 -----PKIDVFAFGVVLIELLTGRKAMTTKENGVEVVLWKDIWKIFD--QEEENRE 516
++DVF+EGVVL+EL++G++A+ E G V LW I + E+ +
Sbjct 495 PEYLADGVVSTRMDVFSFGVVLLELISGKEAV--DEEGRV--LWMSARGILEGKDEKVK 550
Query 517 ERLKKWMDPK--LESYYPIDYALSASLAVNCTADKSLSRPTIAEIVLSL 564
+R+K WMD L +D +++ +A CT RP++ +IV +L
Sbjct 551 KRVDWMDEGLLRESCSMDSVINVMATACTHRDPSKRPSMVDIVYAL 599

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>gb|AAT00791.1| SYM10-like protein [Galega orientalis]
Length=244

Score = 351 bits (901), Expect = 2e-94, Method: Compositional matrix adjust.
Identities = 179/244 (73%), Positives = 204/244 (83%), Gaps = 3/244 (1%)

```

Query 223 VLIPVTRLPVLARSPSDGRKGGIR-LPVIIGISLGCTLLVLVLAVLLVYVYCLMKMTLNR 281
+LIPVT LP L + S G + LPVIIGISLG ++VL + LVYVYCLMK LNR
Sbjct 1 ILIPVTNLPKLDQSSSGSISSSKKLPVIIGISLGSAFFIVVLTLSLVYVYCLMKRLNR 60
Query 282 SASSAETADKLLSGVSGVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVK 341
S S AETADKLLSGVSGVSKPTMYE D IMEAT +LS+QCKIGESVYKANI+ + LAVK
Sbjct 61 STSLAETADKLLSGVSGVSKPTMYEIDVIMEATNDLSQCKIGESVYKANIDSRDLAVK 120
Query 342 RFKEDVTEELKILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFKSCSDTS 401
+ K+D +EELKILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSLD+WLFS++ S TS
Sbjct 121 KIRKADASEELKILQKVNHNGLVKLMGVSSDNDGNCFLVVEYAENGSLDDWLFSEA- SKTS 179
Query 402 NS-RASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMA 460
NS +SLTW QRI +A+DVA+GLQYMHEH YPRI+HR IT+SNIL+DSNEFKAKIANF
Sbjct 180 NSIVSSITWSQRIGIAMDVAVGLQYMHEHTYPRIIHYITTSNILLDSNFKAKIANFLDG 239
Query 461 RTFT 464
+T T
Sbjct 240 KTST 243

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>emb|CB126350.3| unnamed protein product [Vitis vinifera]
Length=595

Score = 345 bits (884), Expect = 1e-92, Method: Compositional matrix adjust.
Identities = 217/575 (37%), Positives = 320/575 (55%), Gaps = 67/575 (11%)

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Query 28 AQSQ-QDNRNRFSCPSD-SPFSCETYTYIAQSPNFLSLTNISNIFTDSPLSIARASNLE 85
+Q+Q + N T + C ++ S C T+ Y A SPNFL L +I ++F S L I+ SN+
Sbjct 27 SQAQPEPNATGYPCSANLSSYPCHTFAFYTATSPNFLDLASIGDLFWVSRLMISEPSNIS 86
Query 86 PMDDKLVKDQVLLVPVTCGC-----TGNRSFANISYEINQGDSEFYFVATTSYENLTNWRA 140
+ LV Q L VP+ C C T S+AN+SY I GD+FY V+T S+ NLT ++
Sbjct 87 SPSNPLVAGQSLFVPLNCSCNSVNTTTAISYANLSYTIKSGDTFYLVSTFSFLNLTYYYS 146
Query 141 VMDLNPVLSPNPKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGA 200
V +NP L P L +G +V+FP+FCCKCP++ QL + +LI+YV++P DN++ V+ G+
Sbjct 147 VEIVNPFLVPTDLDVGDKVIFPIFCCKPNETQLRNGVNFLLISYVFPQSDNLTGVAASLGS 206
Query 201 SPEDIMSENNGQNTAANNLPVLIPVTRLP-----VLARSPSDGRKGGIRLPVIIGIS 254
I+ N G N + +PV+RLP V A + RK R VIIG++
Sbjct 207 DTASIIDVN--GDNIQPFQT--IFVPVSRLENISQPNVTASVATSVRKVE--RKGVIIGLA 261
Query 255 LGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADKLLSGVSGVSKPTMYETDAIMEA 314
+G L L+ LK + +N L++ VS + K +Y + + +A
Sbjct 262 IG--LGDKERPLVGRGTGLKAEENV-----LMADVSDCLDKYKVYGIEELRDA 308
Query 315 TMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHNGLVKLMGVSSD-ND 373
T SE+ I SVYK +I+G++ A+K+ K + EELKILQKVNHNGLV+L G D D
Sbjct 309 TGGFSERSLIQGSVYKGSIDGELYAIKKMKWNAYEELKILQKVNHNGLVLRLEGFCIDPED 368
Query 374 GNCFFVVEYAENGSLDEWLFKSCSDTSNSRASLTWCQRISMAVDVAMGLQYMHEHAYPR 433
C++VE+ ENGL WL + L W R+ +A+DVA GLQY+HEH PR
Sbjct 369 ATCYLVYEFVENGSLQSWLH-----GDRDEKLNWKNRLRIAIDVANGLYIHEHTRPR 421
Query 434 IVHRDITSSNILLDSNFKAKIANFSMARTFTNPM-----PKID 472
+VH+DI SSNILL N +AKIANF +A++ N + ++D
Sbjct 422 VVHKDIKSSNILLDGNMRAKIANFGLAKSGCNAITMHIVGTQGYIAPEYLADGVVSTRMD 481
Query 473 VFAGGVVLIELLTGRKAMTTKENGVEVVLWKDIWKIFD--QEEENREERLKKWMDPK--LES 529
VF+FGVVL+EL++G++A+ E G V LW I + E+ + +R+K WMD L
Sbjct 482 VFSFGVVLLELISGKEAV--DEEGRV--LWMSARGILEGKDEKVKAKRVKDWMDDEGLLRE 537
Query 530 YYPIDYALSASLAVNCTADKSLSRPTIAEIVLSL 564
+D +++ +A CT RP++ +IV +L
Sbjct 538 SCSMDSVINVMATACTHRDPSKRPSMVDIVYAL 572

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>emb|CAN66762.1| hypothetical protein [Vitis vinifera]
Length=591

Score = 338 bits (867), Expect = 1e-90, Method: Compositional matrix adjust.
Identities = 205/567 (36%), Positives = 314/567 (55%), Gaps = 55/567 (9%)

Query 28 AQSQ-QDNRTNFCSPSD-SPPPSCETYVVTYIAQSPNFLSLTNISNIFDTSPLSIARASNLE 85
+Q+Q + N T + C + + S C T + Y A SPNFL L + I + + F S L I + SN+
Sbjct 27 SQAQPEANATGYPCSANLSSYPCHTFAFYTA SPSPNFLDLASIGDLFWFVSRMLMSEPSNIS 86

Query 86 PMDDKLKVKQVLLVLPVTCGC-----TGNRSFANISYEINQGDSEFYFVATTSYENLTNWRA 140
+ LV Q L VP+ C C T S+AN++Y I GD+FY V+T S+ NLT + +
Sbjct 87 SPSPNLVPAQGSFLVPLNCSNVNATTASISANLYTIKSGDTFYFLVSTFSLNLTITYYS 146

Query 141 VMDLNPVLSPKLGPIGIVVFPFLFCCKPSKNQDLKEIKYLIYVWPKPGDNVSLVSKDFGA 200
V +NP L P L +G +V+FP+FCCKP++ Q L + +LI+YV++P DN++ V+ G+
Sbjct 147 VEIVNPFLVPTDLDVGDVKVIFIFCKCPNETQLRNGVNFLLISYVYQPSDNLTLTGAASLGS 206

Query 201 SPEDIMSENNYQGNFTAANNPLVPLIVTRTLPVLAR-----SPSDGRKGIRLPVIGISL 255
I+ N G N + +PV+RLP ++ SP+ + R IIG+S+
Sbjct 207 DTASIIDVN--GDNIQPFQ--IFVPSRLPNISQPNVTASPATSVRRVERKGAIIGLSI 262

Query 256 G---CTLLVLVLAVLLVYVYCL--KMKTL-----NRSASSAETADKLLSGVSGYVS 301
G C L++L+ L VY + + K+K+ R + L++ VS +
Sbjct 263 GLGVCGILVLVLLIGWVYRHVMVEIKIETEGDKERPLVGRSGSLKAAEEVNLMADVSDCLD 322

Query 302 KPTMYETDAIMEATMNLSEQKIGESVYKIANIEGKVLAVKRFKEDVTEELKILQKVNHGN 361
K +Y + + +AT SE+ I SVYK +I+G++ A+K+ K+ EELKILQKVNHGN
Sbjct 323 KYKVYGIEELRDATGGFSEERSLIQGSVYKGSIDGELYAIKKMKWNAYEELKILQKVNHGN 382

Query 362 LVKLGMVSSD-NDGNCFFVVEYAEAGNSLDLEWLFKSKCSDTSNSRASLTWCQRISMAVDVA 420
LV+L G D D C++VYE+ ENGL WL + + L R + +A+DVA
Sbjct 383 LVRLEGFCIDPEDATCYLVYEFVENGSLQSWLH-----GDRDEKLNWKNRLRIAIDVA 435

Query 421 MGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMPKIDVFAFGVVL 480
GLQY+HEH PR+VH+D I SSNILL N +AKIANF +A++ N + +
Sbjct 436 NGLQYIHEH PRVHVHDKISNILLDGNMRKIANFGLKAGSGCN-----AIT 483

Query 481 IELLTGKAMTTKGENGVMLWKDIWKIFD--QEEENREERLKKWMDPK-LESYYPIDYAL 537
+ + + + E G V L W I + E+ + +R+K WMD L +D +
Sbjct 484 MHIVGTQGEKAEVDEGRV--LWMSARGILEGDKKVKAKRVDWMDEGLLRSCSMDSVI 541

Query 538 SLASLAVNCTADKSLSRPTIAEIVLSL 564
++ ++A CT RP++ +IV +L
Sbjct 542 NVMAVATACTHRDPSKRPSMVDIVYL 568

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<http://blast.ncbi.nlm.nih.gov/Blast.cgi>

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Sbjct 73 QTQLQNKVNYLVSYVFPQSDNLSVASTFGVETQSIVDVNGNNIQPYDTIFVPVNQLPQL 132
Query 225 I-PVTRLFVLARSFSDGRKGGIRLPVIGISLGCCTLLVLVLAVLLVYVYCLKMK----- 277
      P +P A P + G+ + + +G+ + LLVLV V LK +
Sbjct 133 AQPVTVVVPSGAPPEKTERKGVIIGLAVGLGIAGLLLVLSGVWFYREGVLKKRRDVEKV 192
Query 278 -----TLNRSASSAETAD-KLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYK 330
      LN + + + L++ VS + K +++ D + EAT SE C I SV+K
Sbjct 193 EEKRRMQNLGGSKGLKDIEVSLMADVSDCLDKYRVFKIDELKEATNGFSENCLIEGVSFK 252
Query 331 ANIEGKVLAVKRFKEDVTEELKILQKVNHGNNLVKLMGVSSD-NDGNCFFVVEYEAENGSLD 389
      +I G+ A+K+ K + EELKILQKVNHGNNLVKL G D D NC++VYE+ ++GSL
Sbjct 253 GSINGETYAIAKKMKWNACEELKILQKVNHGNNLVKLEGFCDPEDANCYLVEYFVDSGSLH 312
Query 390 EWLFSKSCSDTSNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSN 449
      WL N + L+W R+ +A+DVA GLQY+HEH PR+VH+DI SSNILLDS+
Sbjct 313 SWLH-----RNEKEKLSWKTRLRVAIDVANGLYIHEHTRPRVVKDKIKSSNILLDS 365
Query 450 FKAKIANFSMARTFTNPM-----PKIDVFAFGVVLIELLTGRK 488
      +AKIANF +A+T N + +DVF+FGVVL+EL++GR+
Sbjct 366 MRAKIANFGLAKTGCNAITMHIVGTQGYIAPEYLADGVVTRMDVFSFGVVLLELISGRE 425
Query 489 AMTKENGVEVVMWKDIWKIFD---QEENREERLKKWMDPK-LESYYPIDYALSLASLAV 544
      A+ E G+V LW + + + +E + +RL WMD LE ++ + + ++A+
Sbjct 426 AI--DEEGKV--LWAEAIGVLEGNVEERRKVKRLTAWMDKVLLEESCSMESVMNTMAVAI 481
Query 545 NCTADKLSRPTIAEIVLSL 564
      C RP++ +IV +L
Sbjct 482 ACLHRDPSKRFSMVDIVYAL 501

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>emb|CA002950.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=243

Score = 313 bits (801), Expect = 6e-83, Method: Compositional matrix adjust.
Identities = 158/245 (64%), Positives = 191/245 (77%), Gaps = 3/245 (1%)

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Query 54 YIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFAN 113
      Y AQSPNFLSL+NIS+IF+ SPL IA+ASN+E D KL+ DQ+LLVPVTCGCT N SFAN
Sbjct 1 YRAQSPNFLSLSNISDIFNLSPRIAKASNIEAEDKKLIPDQLLLVPTVTCGCTKNHSFAN 60
Query 114 ISYEINQGDSEFYFVATTSYENLTNWRAVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQL 173
      I+Y I QGD+F+ ++ TSY+NLTN+ + NP LSP LP+ +V PLFCKCPSKNQL
Sbjct 61 ITYSIKQGDNFFILSITSYQNLNTNYLEFKNFNPNSPTLLPLDTKVSVPFLFCKCPSKNQL 120
Query 174 DKEIKYLITYVWKPGDNVSLVSKFGASPEDIMSENNYQGNFTAANNLPVLIPVTRLPV 233
      +K IKYLITYVW+ DNV+LVS KFGAS ++++ENN+ NFTA+ N VLIPVT LP L
Sbjct 121 NKGIKYLITYVWQDNQDNVTLVSSKFGASQVEMLAENNH--NFTASTNRSVLIPTVSLPKL 178
Query 234 ARSPSDGRKGGIR-LPVIIGISLGCCTLLVLVLAVLLVYVYCLKMKTLNRSASSAETADKL 292
      + S+GRK + L +IIGISLG +LVL + LVYVYCLKMK LNRS SS+ETADKL
Sbjct 179 DQPSNGRKKSSSQNLALIIGISLGSAFFILVLTLSLVYVYCLMKRLNRSSTSSSETADKL 238
Query 293 LSGVS 297
      LSGVS
Sbjct 239 LSGVS 243

```



>gb|EAY87082.1| hypothetical protein OsI_08480 [Oryza sativa Indica Group]
Length=651

Score = 313 bits (801), Expect = 6e-83, Method: Compositional matrix adjust.
Identities = 205/601 (34%), Positives = 310/601 (51%), Gaps = 85/601 (14%)

```

Query 37 NFSCPSDSPSPSCETYVTYIAQSPNF-LSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQ 95
      F+C +++ C Y Y A L I ++F S +A A+NL L Q
Sbjct 39 GFNCTANATYPCPAYALYRAGFGGVPLEFAAIGDLFAASRFMVAHANLS-TSAVLAARQ 97
Query 96 VLLVPVTCGCTGN--RSFANISYEINQGDSEFYFVATTSYENLTNWRAVMDLNPVLSPNKL 153
      LLVP+ CGC ++A + Y+IN GD+++ V+TT +NLT ++AV +NP L P L
Sbjct 98 PLLVPLQCGCPSPSRPNAYAPMQYQINAGDTYWIIVSTTKLQNLQYQAVERNVPTLVPTNL 157
Query 154 PIGIQVVFPLFCKCPSKNQLDKEIKYLITYVWKPGDNVSLVSKFGASPEDIMSENNYGO 213
      IG V FP+FC+CP+ + L+TYV +PGD + ++ F + ++S N Q
Sbjct 158 DIGQIVTFPIFCQCPA---EDNATALVTYVMQPGDTYASIAATAFAVDAQSLVSLNGPEQ 214
Query 214 NFTAANNLPVLIPVTR-----LPVLAR-----SPSDGRKGGIRLPVII----- 251
      ++ +L+P+ R LP + R +P+ P ++
Sbjct 215 GTRNLSSPEILLVPLRRQVPEWLPPIVRVNNISTTPASPPPSNTPAFTVVSNNRDGVVTGL 274
Query 252 GISLGCCTLLVLVLAVLLVYVYCLKMKTLNRSASSAETADK----- 291
      I LG + +L +LL+ ++K R A + + D
Sbjct 275 AIGLGVVGGLWLLQMLLGLWRRLKARGRAEAVASGDGGEGGRFKAASGGGGGGGGG 334
Query 292 --LLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTE 349
      L+S +S ++ K +++ + + T ++ I SVYKA I+G+V AVK+ K D E
Sbjct 335 RFLVSDISEWLDKYKVKFVEELESCTGGFDDEHLIQGSVYKAYIDGEVFAVKMKWDACE 394
Query 350 ELKILQKVNHGNNLVKLMGVSSDND-GNCFVVEYEAENGSLDEWLFSKSCSDTSNSRASLT 408
      ELKILQKVNH NLVKL G +++ G+C++VVEY ENGSLD WL +R L
Sbjct 395 ELKILQKVNHSNNLVKLEGF CINSETGDCYLVEYEVENGSLDLWLM-----DRDRAR-RLD 448
Query 409 WCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNFP-- 466
      W R+ +A+D+A GLQY+HEH +PR+VH+DI SSN+LLD +AKIANF +A+T N
Sbjct 449 WRARLHIALDLAHLGLYIHEHTWPRVVKDKIKSSNVLLDDRMRAKIANFGLAKTGHNAV 508
Query 467 -----MMPKIDVFAFGVVLIELLTGRKAMTTKENGVEVVMWKDI-W 506
      + K+DVFA+GVVL+EL++GR+A+ + +GE LW D
Sbjct 509 THIVGTQGYIAPEYLADGLVTTKMDVFAYGVVLELVSGREAV-SDDSGE--PLWADADE 565
Query 507 KIFDQEENR-EERLKKWMDPKL-ESYYPIDYALSLASLAVNCTADKLSRPTIAEIVLSL 564
      ++F E R E R+ WMDP L E P S+ S+A C RP++ ++ +L
Sbjct 566 RLFRGREERLEARVAWMDPALAEQTCPGVSASVSVAKACLRDPAKRFSMVDVAYTL 625
Query 565 S 565
      S
Sbjct 626 S 626

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>ref|XP_001767824.1|  predicted protein [Physcomitrella patens subsp. patens]
 gb|EDQ67338.1|  predicted protein [Physcomitrella patens subsp. patens]
 Length=658

GENE ID: 5931014 PHYPADRAFT_132645 | hypothetical protein
 [Physcomitrella patens subsp. patens] (10 or fewer PubMed links)



Score = 302 bits (774), Expect = 8e-80, Method: Compositional matrix adjust.
 Identities = 211/624 (33%), Positives = 319/624 (51%), Gaps = 84/624 (13%)

Query	26	IVAQQQDNRTNFCSPSPSPSCETYVITYIAQSPNFLSLTNISNIFDTSPLSIARASNLE	85
		I AQ Q N + ++ C + C+TY Y +LT+I +F+TS IA AS+++	
Sbjct	24	ISAQQQYRNTSGYTCSGTT--RCQTYAFYRTAGSQS-TLTSIVTLFNTSVEGIATASDVD	80
Query	86	PMDDKLVKDQ-VLLVPVTCGCTGNRSFANISYEINQGDSFYFVATTSYENLTNWRAVMDL	144
		P D+ L +P+ C C N A S +I GD+ Y A +Y+ LT W A+	
Sbjct	81	PNRTIPFNDRDPLIYIPLNCSFNNTRFALTSQQIKSGDTMYKFANGTYQGLTTWEAISVA	140
Query	145	NEVLSPNKLPIGIQVFPFLFCKCPSKNQLDKEIKYLITYVWKPGDNVSLVSKFGASPED	204
		NP + + +G +V PL C CP+ Q + +LT+Y B + + +S F +	
Sbjct	141	NPTVIIITNMTVG DYLVIPLRACAPTTTQRRAGSRILLTYSIFPDET LKFISGLFNIPVE	200
Query	205	IMSENNYQG--NFTAANN----LPVLIPVTRLPVLARSP----SDGRKGGIRLPVI----	250
		+ + NN N A N LP L+P++ + + P + G +PVI	
Sbjct	201	LQTANNGASSANLAAFTLLVPLPSLVPLSTMKFSPFPFPPSVEAPGPAPSTLPVITNKD	260
Query	251	-----IGISLGCTLLVLVLAVLLVYVYCLMKMT-----LNRSAS-----	284
		IGI G + LA +L V C +K LNR +S	
Sbjct	261	PSKTSMYIGIVFGG--FGMALAFILACVLCATVKRYKNIIRKIEYENRGLLNKSSVTDI	318
Query	285	-SAETAD-KLLSGVSGYVS--KPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLA	340
		S +TA+ L+SG++ K T + + + AT + SE +I SV+ A + G +A+	
Sbjct	319	DSLDTANSLSVSGMTDLFGCDKLTKFSEELDTATNHFSEDNRIQGSVFLAKNGSFVAI	378
Query	341	KRFKEDVTEELKILQKVNHNGLVLMGV-SSDNDG---NCFVYIEYAENGSLDEWLFSKS	396
		KR K ++++ELKIL +V+HGN+VKL+G+ + D+DG N ++VYIEYAENGSL + L +	
Sbjct	379	KRMKGNMSDELKILSQVHHGNVVKLVGMCARDSGRSENLYIVYIEYAENGSLSDCLHHQM	438
Query	397	CSDTNSNRAS---LTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAK	453
		TSN S L W R+ +AVD+A GL+Y+H + P +VH+D+ SSNILLD NF+AK	
Sbjct	439	AYPTSNFSRSVGLLIWNTRMQIAVDIASGLEYLHNYTNPSLVHKDKVSSNILLDKNFRAK	498
Query	454	IANFSMARTFTN-----PMM-----PKIDVFAFGVVLIELLTGR	487
		+ANF MA+ + P+M K DVE+FGVVL+ELL+GR	
Sbjct	499	VANFGMAKPADSGEPGLMTEHIVGTQGYMAPEYLEHGLVSTKADVFSFGVVLLELSGR	558
Query	488	KAMTTKENGVEVVMWKDIWKIFDQENREERLKKWMDPKLESYYPIDYALSASLAVNCT	547
		+A+ GE ML I + ++ + +L+ WMDP+L++ YP D ALS+A LA +C	
Sbjct	559	EAICNDGGEFTMLSATISNVLSGDD-QMAKLQAWMDPRLQNAYPSDIALSVAILAKSCV	617
Query	548	ADKSLSRPTIAEIVLSLSLLTQPS 571	
		SRP + +I +LS ++ S	
Sbjct	618	ETDPRSRPDMKQISFALSKMSSAS 641	

>dbj|BAI79278.1| LysM type receptor kinase [Lotus japonicus]
 Length=666



Score = 297 bits (761), Expect = 2e-78, Method: Compositional matrix adjust.
 Identities = 189/631 (29%), Positives = 327/631 (51%), Gaps = 88/631 (13%)

Query	14	ILCLVIMLFSTNIVA-QSQQD--NRTNFCSPS-----DSPPSCETYVITYIAQSPN	60
		+L ++I+ FS I + Q+QQ+ N C + +S SC++Y+T+ + SP	
Sbjct	18	LLLVMIISFSHMTFSTQAQQEYVNNKQLDCDTQYNTTYGNVCNSVTSCQSYLTFKSSPE	77
Query	61	FLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQ	120
		+ + ++IS + ++P +A+++N+ + ++ D ++ VPVTC C+G R N +Y + +	
Sbjct	78	YNTSSSYLLNSTPSPSLVAKSNNTDVT-PIITDTMTVTPVTCSCSGGRYQHNAATYLNKK	136
Query	121	-GDSFYFVATTSYENLTNWRAVMDLNPVLSPNKLPIGIQVFPFLFCKCPSKNQLDKEIKY	179
		G++++ +A +Y++LT +A+M NP + N L G + PL C CP+K Q D KY	
Sbjct	137	TGTYFYSIANNTYQSLTTCQALMAQNPDYDAKN-LFAGDDLHVPLRCACPTKKQSDAGFKY	195
Query	180	LITYVWKPGDNVSLVSKFGASPEDIMSENNYQGNFTAANNLPVLI PVTRLP-----	231
		L+TY+ G++ +++ FG + ++ N P+L+P+ P	
Sbjct	196	LLTYLVSQGESPDIAEIFGVDTQSVLDANELDSKSVVFYFTPLLVLKTEPPARLQIAA	255
Query	232	-----VLARSPDGRKGGIRLPVIIGISLGCTLLVLVLAVLLVYVYCL-----	274
		+ + VI+G+++G + +V LLV+ C	
Sbjct	256	SPFESPPPAPAGNDSSSSSKKVVIVGTVGVAVCLV--ALLVFFLCFYNRRRRQPAPPP	313
Query	275	-----KMKTLNRSASSAETADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIG	325
		+K ++ + +E+ GV + T Y+ I AT SE+ KI	
Sbjct	314	VSVKDFPDSAVKMVSETTPTTESWSLSSEGVRYAIESLTAYKFGDIQTATKFFSEENKIK	373
Query	326	ESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHNGLVLMGVSSDNDGNCVYIEYAEN	385
		SVY+A+ +G AVK DV+ E+ +L+++NH N+++L G + GN ++VYE+AE	
Sbjct	374	GSVYRASFKGDDAAVKILNGDVSAEINLLKRINHANIIRLSGFCV-HKGNTYLVYEFAN	432
Query	386	GSLEWLFSKSCSDTSNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILL	445
		SLD+WL S S SL+W QR+ +A DVA L Y+H + P +H+++ S N+L	
Sbjct	433	DSLDDWLHSDKKYQNS---VLSWMQVRQIAYDVADALNYLHNYTNPIHIHKNLKSNGVL	489
Query	446	LDSNFKAKIANFSMARTFTNP-----MMPKIDVFAFG	477
		LD F+AK++NE +AR + + PK+DVFAFG	
Sbjct	490	LDGKFRKAVSNFGLARVMEDQGEDGGFQMTRHVVGTVGQYMPPEYIESGLITPKMDVFAFG	549
Query	478	VVLELTTLGRKAMTTKEN---GEVVMWLKDIWKIFDQENREERLKKWMDPKLESYYPID	534
		VV++ELL+GR+A ++ E GE ML + + + +N ++L+ +MDP L YP+D	
Sbjct	550	VVMLELLSGREATSSGEKNGLGGENKMLSETVNHVL-EGDNVRDKLRGFMDFTLRDEYPLD	608
Query	535	YALSASLAVNCTADKSLSRPTIAEIVLSLS 565	
		A S+A +A C A SRP I+E++++LS	
Sbjct	609	LAYSMAELIAKRCVAHDLNSRPNISEVIMTSL 639	

>ref|XP_002326901.1|  predicted protein [Populus trichocarpa]
 gb|EEE73651.1|  predicted protein [Populus trichocarpa]
 Length=609
GENE ID: 7470467 POPTRDRAFT_591844 | hypothetical protein [Populus trichocarpa]
 (10 or fewer PubMed links)

Score = 292 bits (748), Expect = 8e-77, Method: Compositional matrix adjust.
 Identities = 185/555 (33%), Positives = 301/555 (54%), Gaps = 52/555 (9%)

Query	47	SCETVYTYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLKVDQVLLVPVTCGCT	106
		SC+ ++ + +Q P+F S+ +IS + + +AR +N+ + + ++V+ VPV C C	
Sbjct	54	SCQAFILFKSQ-PSFNSVPSISALTSANQEELARINNVTRLSEFPTNNEVI-VPVNCFCF	111
Query	107	GNSRFANISYEINQG-DSFYFVATTSYENLTNWRVMDLNFVLSPNKLPIGIQVVFPLFC	165
		G AN + ++ ++Y +A +YE L+ A+ LN + + LP G ++ PL C	
Sbjct	112	GQYYQANTTIQVTTTRGTYYVIANETYEGLSTCAALKHLNIHGEYDLLP-GEELQVPLRC	170
Query	166	KCPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNGQNFATAANNLPVLI	225
		CP+ NQ+ + KYL+TY DN+ ++D+F S +DI+ N +N T + +LI	
Sbjct	171	ACPTTNQIRGKTLYLVTYPLSSDDNIPDIADRFKVSTKDILDANGMEENPTLYPDTTILI	230
Query	226	PVTRLPLVARS-----PS----DGRKGGIRLPVIGISLGCTLLVLVLAVLLVYV	271
		P+ P +++ PS R + G++ C+LLV+ + +V++	
Sbjct	231	PLPTQPTSSQTIIHSNPNISPPSALSPRNRGSKKKHYESAGLAAACSLLVISITAVVFL	290
Query	272	YCLKM--KTLNRSASSAETA-DKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESV	328
		C K K R R + + + ++ Y +++ + +AT NLS + +I SV	
Sbjct	291	SCKKTRKVKSGRGRRERQAVPEDIRVEIASYEQVLKVKFEEVRKATENLSSESRRNGSV	350
Query	329	YKANIEGKVLAVKRFKEDVTEELKILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSL	388
		Y+ G++LAVK+ DVT+E+ IL+++NH NL+KL GV +N G ++V EY ENGSL	
Sbjct	351	YRGEFGGEILAVKKMSRDVTEKEVNILKRINHFNLIKLEGVCE-ENRGCFYLVLEYMENGSL	409
Query	389	DEWLFSKSCSDTNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDS	448
		EWL K +T N W QRI +A+DVA GL Y+H P VH+DI SSN+LL+	
Sbjct	410	REWLSCKKFEETGN-----WAQRIQIALDVANGLYLHSFTEPAYVHKDIKSSNVLLNG	463
Query	449	NFKAKIANFSMARFTFTNPM-----PKIDVFAFGVVLIELLTG	486
		N +AKIANFS+AR T+ M PKIDV+AFGV+L+EL+TG	
Sbjct	464	NLRKAKIANFSLARAATSAAAMTKHVVGSIGYMAPEYVREGQVTPKIDVYAFGVILLELITG	523
Query	487	RKAMTTKENGEEVVMLWKDIWKIFDQENREERLKKWMDPKLESYYPIDYALSASLAVNC	546
		+ A+ T ++G +L +I+ I + +N E L ++DP L+ ++AL LA ++V C	
Sbjct	524	KDAVFT-QDGREALLSTEIFSIMEN-KNPEVELDFVDPAKLGSCGTNFALCLAKVSVAC	581
Query	547	TADKSLSRPTIAEIV 561	
		+ RP++ E+V	
Sbjct	582	LMKEPARRPSMEEVV 596	

>ref|XP_001783589.1|  predicted protein [Physcomitrella patens subsp. patens]
 gb|EDQ51621.1|  predicted protein [Physcomitrella patens subsp. patens]
 Length=637

GENE ID: 5946784 PHYPADRAFT_152558 | hypothetical protein
 [Physcomitrella patens subsp. patens] (10 or fewer PubMed links)

Score = 291 bits (744), Expect = 2e-76, Method: Compositional matrix adjust.
 Identities = 194/611 (31%), Positives = 312/611 (51%), Gaps = 73/611 (11%)

Query	27	VAQSQQDNRTNFSC-PSDSPSCETVYTYIAQSPNFLSLTNISNIFDTSPLSIARAS--N	83
		+AQ ++ ++C + S SC T+ Y SL + + F+ + ++A S N	
Sbjct	1	MAQQNYNDTEGYACNAAPSSSTSCSTFAFYRTFQAG-ESLRKVGDFNKTAAAVANVSGMN	59
Query	84	LEPMDDKLKVDQVLLVPVTCGCTGNRSFANISYEINQDGSFYFVATTSYENLTNWRVMD	143
		L L + Q L VP+ C C RS +S+ I +GD+F+ ++ T Y LT ++A+M	
Sbjct	60	LLSTTASLKQTQALYVPLDCRCLNARSQMVSHTIVKGDTFWLLSVTEYGGGLTRYQAMMA	119
Query	144	LNPFVLSPNKLPIGIQVVFPLFCCKCPKSNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPE	203
		NP L IG + P+FC CP+ Q+ YL+T P + + ++S +FG S	
Sbjct	120	SNPSKDVYNIITIGDTITVTPIFCACPTAAQVANGTNYLVTTTVYPSETLDIISARFGISTT	179
Query	204	DIMSENNGQNFATAANNLPVLI PVTRLPLVAR-----SPSDG	240
		D+ NN + + N +L+P+ LP LA +P+	
Sbjct	180	DLSRANNVNSSSILDVNTTLLVLPLATLPPLATMDWAPVTSQPPPSPPATVASPNAAPAVI	239
Query	241	RKGGIRLPVIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSASSAETADK-----LL	293
		K + P+ IGI++G L L L+ ++ + + E + LL	
Sbjct	240	TKSASQTPLYIGIAGVAFGLTLAAVFALLLLFKASRNSGKPKDLTEEMKRPNMVHLELL	299
Query	294	SGVSGYVS--KPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEEL	351
		+G+S V KP + + I AT S + I SVYK I G+++A+K+ K ++T+EL	
Sbjct	300	AGMSDMVGSEKPVLLSHHEETQSATQGFSPENFIQGSVYKGCINGQLVAIKQMKGNMTQEL	359
Query	352	KILQKVNHNGLVVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSKSC---SDTNSRASLT	408
		KIL +V+H NLVKL+G+ N ++VVEYA++GSL++ L +++ + S A L	
Sbjct	360	KILCQVHHSNLVKLVGLCVGGSSENLVLYEYAKHGSINDCLRNQAAIGRTTFSQSAAYLP	419
Query	409	WCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARFTTNP--	466
		WC R+ +A+DVA GL+Y+H + P VH+D+ +SNILLD NF+AK+ANF MA++ +	
Sbjct	420	WCSRVRIALDVASGLEIYHNYTNPSFVHKDVKTSNILLDENFRKAVANFGMAKSAASADA	479
Query	467	-----MMP-----KIDVFAFGVVLIELLTGRKAMTTKENGEEVVMLW	502
		M P K DV+AFGVV++E+L+G++A+ E E	
Sbjct	480	GPLLTRHITGTQGYMAPEYLEHGLVTVKADVAFGVVVLIELSGKEAVVRPEKDEEEQGV	539
Query	503	KD-----IWKIFDQ--EENREERLKKWMDPKLESYYPIDYALSASLAVNCTADKSLSR	554
		K+ I + + + E + E+L+K++DP+L S YPI+ A S+ASLA+ C R	
Sbjct	540	KERALSDIIVDVINAGTAELQTEQLRRFIDPQLHSAYPIEIIASSIASLAMTCDIDPDPAVR	599
Query	555	PTIAEIVLSLS 565	
		P++ ++ +LS	
Sbjct	600	PSMKDVTFFALS 610	

>dbj|BAI79277.1| LysM type receptor kinase [Lotus japonicus]
 dbj|BAI79287.1| LysM type receptor kinase [Lotus japonicus]
 Length=667

Score = 286 bits (733), Expect = 4e-75, Method: Compositional matrix adjust.
 Identities = 173/591 (29%), Positives = 309/591 (52%), Gaps = 76/591 (12%)

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Query  43  DSPPSCTTYVYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVT 102
          +S SC++Y+T+ +SP + + +IS + + +P +A++N+ + + +D ++ VPVT
Sbjct  57  NSVTSCQSYLTFKSSSPYNTPTSSISYLLNSTPSLVAKSNNTDVT-PIITDTMVTVPVT 115

Query  103  CGCTGNRSFANISYEINQ-GDSFYFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVF 161
          C C+G R N +Y + + G++++ +A +Y++LT +A+M NP + N L G +
Sbjct  116  CSCSGGRYQHNATYNLKKTGETYFSIANNTYQSLTTCQALMAQNPHYDAKN-LFAGDDLHV 174

Query  162  PLFCKCPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANL 221
          PL C CP+K Q D KYL+TY+ G++ + + + FG + + + N
Sbjct  175  PLRCACPTKKQSDAGFKYLLTYLVSQGESPDZIAEIFGVDTQSVLDANEELDSKSVVYFFT 234

Query  222  FVLIPVTRLPL-----VLARSPSDGRKGGIRLPVIIGISLGCTLLVLVLAVLL 268
          P+L+P+ P + + + + VI+G+++G + + +V LL
Sbjct  235  PLVLPLKTEPPARLQIAASPPESPAPAGNDSSSSSKWVIGVTVGVAVCLVV--ALL 292

Query  269  VYVYCL-----KMKTLNRSASSAETADKLLSGVSGYVSKPTMYE 307
          V+ C +K ++ + + E+ + + + + T Y+
Sbjct  293  VFFLCFYNNRRRQPAPPPVSVKDFPDSAVKMWSETTPTTESWSLSSEGVRYAIESLTAYK 352

Query  308  TDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNIKLVKMG 367
          I AT SE+ KI SVY+A+ +G AVK DV+ E+ +L+++NH N+++L G
Sbjct  353  FGDIQTATKFFSEENKIKGSVYRASFKGDDAAVKILNGDVSAEINLLKRNHANIIRLSG 412

Query  368  VSSDNDGNCVFVVEYAENGSLDEWLFKSKCSDTSNSRASLTWCQRISMAVDVAMGLQYMH 427
          + GN ++VYE+AEN SLD+WL S+ S SL+W QR+ +A DVA L Y+H
Sbjct  413  FCV-HKGNTRYLVVEFAENDSLDLHLHSEKKYQNS---VLSWMQVRVQIAYDVADALNYLH 468

Query  428  EHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNP----- 466
          + P ++H+++ S N+LL+ F+AK++NF +AR +
Sbjct  469  NYTNPVLIHKNLKSQNVLLNGKFRKAVSNFGLARAMEQDQGEDGGGFQMRHVVGTVQGYMP 528

Query  467  -----MMPKIDVFAFGVVLIELLTGRKAMTTKEN---GEVVMLWKDIWKIFDQE-EN 514
          + PK+DV+AFGVV++ELL+G++A + GE ++L + + + + +N
Sbjct  529  PEYTENGLITPKMDVYAFGVVMLELLSGKEATGNGDKNGLGKVMVLSQVNHVLEGNDN 588

Query  515  REERLKKWMDPKLESYYPIDYALSASLAVNCTADKSLSRPTIAEIVLSLS 565
          ++L+ +MD L YP+D A S+A +A C A SRP I+E+ ++LS
Sbjct  589  VRDKLRGFMQDQLRDEYPLDLAYSMAEIAKRCVAHDLNSRPNISEVFMTLS 639

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>ref|XP_002510756.1| kinase, putative [Ricinus communis]

gb|EEF52943.1| kinase, putative [Ricinus communis]
 Length=634

GENE ID: 8269969 RCOM_1602540 | kinase, putative [Ricinus communis]

Score = 283 bits (724), Expect = 5e-74, Method: Compositional matrix adjust.
 Identities = 182/572 (31%), Positives = 289/572 (50%), Gaps = 74/572 (12%)

```

Query  47  SCETVYVYIAQSPNFLSLTNISNIF---DTSPLSIARASNLEPMDDKLVKDQVLLVPVTC 103
          SC++Y+T+ + P + + IS +F D++ L IA +N+ + + L +PV C
Sbjct  56  SCQSYLTFRSAPPYYTTPVTISYLFSLQDSASL-IASLNNISSDVSSIIPPQSQLFIPVNC 114

Query  104  GCTGNRSFA-NISYEINQGDSFYF-VATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVF 161
          C G + + N SY + YF VA +Y+ L+ +A+M NP N L +G+++
Sbjct  115  SCFGQYQHNASYTLKFSSETYFSVANDTYQGLSTCQALMSQNPYGDNRN-LSVGMRLQV 173

Query  162  PLFCKCPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANL 221
          PL C CP+ NQ +YL+TY+ GD +S + + + FG P+ I+ N
Sbjct  174  PLRCACPTSNQTAGLFYLLTYMVTWGDITSSIAELFGVRFQSIILDAQLSSTSIIFFPT 233

Query  222  FVLIPVTRLPLVLAR-----SPSDGRKGGIRLPVIIGISLGCTLLVLVLAVLL 268
          P+L+P+T P + + + + P G R +G+ LG LL++
Sbjct  234  PIVLPLTTPPTTKASPPPPVVSPPPLTPVLPSSGSSRKWTYVGVGLGAALLLIFAVSGF 293

Query  269  VYVY----CLKMKT-----NRSASSAETADKLLSGVSGYVSKPTMYETDAIMEAT 315
          ++ Y K+ T+ + SA + + + G + T+Y+ + AT
Sbjct  294  LEWYPKSKSKLTTVPIPSKALQSDSSAVPPDSSTPWSRSAYGVIESLTLTKFHDQLAT 353

Query  316  MNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNIKLVKMGVSSDNDGN 375
          SE+ +I SVYK + +G AVK K DV+ E+ IL+K+NH N+++L GV D N
Sbjct  354  DYFSEKNRIKGSVYKGSFKGDAAAVKVMKGDVSEISILKKINHSNIIRLSGVCL-YDAN 412

Query  376  CFVVEYAENGSLDEWLFKSKCSDTSNSRASLTWCQRISMAVDVAMGLQYMHHEHAYPRIV 435
          ++VYE+AENGSL E + +LTW QR+ +A DVA L Y+H + P +
Sbjct  413  TYLVYEFAENGSLAE-----NVQTLTWKQVRVQIAHDVADALNYLHNYTNPYYI 460

Query  436  HRDITSSNILLDSNFKAKIANFSMARTFTNP-----MM 468
          H+++ +SNILLD+N +AKIANF +ART N +
Sbjct  461  HKNLKTSNILLDANMRAKIANFGLARTLQNEAEGGLHLTRHVVGTVQGYMAPEYMENGVI 520

Query  469  PKIDVFAFGVVLIELLTGRKAMTTKENGVEVVMLWKDIWKIFDQEEENREERLKKWMDPKLE 528
          PK+DVFAFGVV++ELL+G++A T +N ML I ++ + +N +L +MDP L
Sbjct  521  PKLDVFAFGVVI LELLSGKEAATYDKNAREEMLSASICRVL-EGDNVVRHKLCGFMDPSLG 579

Query  529  SYYPIDYALSASLAVNCTADKSLSRPTIAEI 560
          YP+D A SLA LA C + +RP++++
Sbjct  580  KQYPLDLAFSLAQLAQTCISHDINARPSVSQV 611

```

>ref|XP_002522569.1| BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]

gb|EEF39869.1| BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]
 Length=624

GENE ID: 8259229 RCOM 1014860 | BRASSINOSTEROID INSENSITIVE 1-associated
receptor kinase 1 precursor, putative [*Ricinus communis*]

Score = 280 bits (717), Expect = 3e-73, Method: Compositional matrix adjust.
Identities = 179/568 (31%), Positives = 303/568 (53%), Gaps = 56/568 (9%)

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Query  47  SCEFYVYIIAQSPNFLSLTNISNIFDTSPLS--IARASNLEPMDDKLVKDQVLLVPVTCG  104
          SC++Y+T+ A  P + S  I  +  +  +  IA +N+  +  ++ ++VPV C
Sbjct  56  SCQSYITFRANPP-YNSPAKIGYLLGSQSEATLIASMNNISCDVATIPTNKQVVVPVNC  114

Query  105  CTGNRSFA-NISYEI-NQGDSFYFVATTSYENLTNWRAVMDLNPVLSPNKLPIGIQVVPF  162
          C  +  N +Y I ++ ++++ +A +Y+ LT  +++ + NP  N+L  G  +  P
Sbjct  115  CHAGLYYQHNAFYRIKDENEYFTLANDTYQGLTTCQSLWEQNF-YDLNELYAGSDLHVP  173

Query  163  LFCKCPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYGQNFATAANNLP  222
          L C CP+ NQ  +K ++TY+  GD +SL+++ F A+ + ++  N  ++  P
Sbjct  174  LRCACPTPNQTASGVKCMLTVMVTWGDYISLIAELFNANEQSVLDANELLEDDLIYPFTP  233

Query  223  VLIPVTRLP----VLARSPSDGRKGGIRL-FV-----IIGISLGCTLLVLV-LAV  266
          L+L+P+  P  +  SP  R  +  +  PV  G  +G  LLVLV  +
Sbjct  234  ILVPLLSEPTVDLPGYSPPTRTPPVEVFPVTESSNKKWVFFGTGIGAVLLVLVAFSA  293

Query  267  LLVYVYCLMKMTLNRSASSAETADKLLS--GVSGYVSKPTMYETDAIMEATMNLSEQCKI  324
          + +C +  ++ ++ +T  +S  G+ ++  +Y+ D+I  AT N SE  ++
Sbjct  294  FSWYFCRRPSQKSQEPNATKTDPSVSVHVGIEFFIESLIYKFDSIQATGNFSEDNRV  353

Query  325  GESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNNLVKLMGVSSDNDGNCFFVVEYAE  384
          SVYK  EG  AVK  + DV+ E+ IL+K+NH N+V+L G  ++GN ++VY+YAE
Sbjct  354  KGSVYKGIPEGDHAAVKAMRGDVSSEIDILKMMNHSNIVRLSGFCV-HEGNTYLVYQYAE  412



Query  385  NGSLEWLFSKSCSDTNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNI  444
          NGSLD+WL  S  +SL+W QR+ +A +VA  Y+H +  P  VH+++T+SNI
Sbjct  413  NGSLEDDLHLHYKNDPVS---SSLWKQLQIAYNVADAFYTLHNYTTPPFVHKNLTSNI  469

Query  445  LLDNFKAKIANFSMARTFTNP-----MMPKIDVFAFG  477
          LL  NF+A I NF +AR  +N  +  PK+DVFA+G
Sbjct  470  LLHGNFRAMTINFLGARKLSNDDQGAQPLTRHVVGTVNGYMAPEYLENGLITPKLDVFAYG  529

Query  478  VVLIELLTGRKAMTTKENGVEVVMWKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYAL  537
          VV++ELL+G+KA+ ++ NGE  ML+  I  +  + +N  E+LK ++DP L  P+ +A
Sbjct  530  VVILELLSGKAVMSE+NGEEKMLFALINNVL-EGDNVREKLKAFIDPCLRGNIPLHFAF  588

Query  538  SLASLAVNCTADKSLSRPTIAEIVLSLS  565
          S+A LA +C A  RP++ E+ +SLS
Sbjct  589  SIAQLAKDCVAHPDNDPFSMLEVFMSSLS  616

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>ref|XP_002990805.1|  hypothetical protein SELMODRAFT_11326 [Selaginella moellendorffii]
gb|EFJ08078.1|  hypothetical protein SELMODRAFT_11326 [Selaginella moellendorffii]
Length=539

GENE ID: 9659107 SELMODRAFT_11326 | hypothetical protein
[Selaginella moellendorffii]

Score = 280 bits (717), Expect = 3e-73, Method: Compositional matrix adjust.
Identities = 190/552 (34%), Positives = 295/552 (53%), Gaps = 31/552 (5%)

```

Query  38  FSCPSDSPSCETVYIIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVL  97
          +SC S+S  SC+ Y  Y A  +  +L ++  F  S  +A AS +  LV DQVL
Sbjct  1  YSCVSNST-SCQAYAAAYRALQGD--TLQSVGLRFRLSVEQLAEASQI-AQSATLVDPQVL  56

Query  98  LVPVTCGCTGNRSFANISYEINQGDSFYFVATTSYENLTNWRAVMDLNPVLSPNKLPIGI  157
          L+P+ C C PS  RS  N +Y I  GD+ Y V+  +++ LT ++AV  NP+  P  L  G
Sbjct  57  LIPLNCSCASGRSQFNATYIIQSGDTLYLVSNGTFFQGLTTYQAVERANPLAVPTNLQPGD  116

Query  158  QVVFFPLFCCKPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYGQNF  217
          +VFP+ C CPS  Q+  +  L+TY  PG+ +  ++  +  S  + S+N  + T
Sbjct  117  SIVFPIRCACPSAQAAGVTSLVYTSIWPGEILDGIARAWNVSRTRLASDNTVSGSATL  176

Query  218  ANNLPVLIPTVRLPVLARSPSDGRKGGIRLFPVIGISLGCTLLVLVLAVLLVYVYCLMK  277
          +  P  +  S  +  +GI++ C  VL++ V LV  Y  +  +
Sbjct  177  SPAAPPPANNPPNNSPSPDSSSSSGSNTGM--YVGIACVAAVLLVVVALVIFYRRRSR  234

Query  278  TLNRSASSAETADK-----LLSGVSGYV--SKPTMYETDAIMEATMNLSEQCKIGESV  328
          + +++S AE +  +  LL+G+ G V  +P ++  +  +AT N S  I  SV
Sbjct  235  KVTKASSYAEPSKQPSPHAPLLAGMHGLVDSERPVVSFYEELCDATNNFSASHLIQGSV  294

Query  329  YKANIEGKVLAVKRFKEDVT-EELKILQKVNHGNNLVKLMGVSSDNDGNCFFVVEYAE  387
          Y+  +  +++A+K  K  T  +ELKIL KV+H NLVKL+G+ S +D  F+VVEYA+NGS
Sbjct  295  YRGILRKQLVAIKEMKGGTTSQELKILCKVHNSNLVKLIGICSGDD-KLFLVVEYADNGS  353


Query  388  LDEWLFSKSCSDTNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILL  447
          L  SC  A+  W  R+ +A+DVA GL+Y+H++  P  VH+D+  SSNILL
Sbjct  354  L-----SSCLHNRTPAATAIWNTRLQVAMDVATGLEYIHDTKPSFVHKDVKSSNILL  407

Query  448  SNFKAKIANFSMARTFTNP--MMPKIDVFAFGVVLIELLTGRKAMTTKENGVEVVMWKDI  505
          +N +AK+ANF MAR +  +  K+DV+AFGVVL+EL  TGR+A+  +  G  D
Sbjct  408  ANLRKAVANFGMARLYLTHGFVTTKVDVYAFGVVLELFTGREAILSTGTGSEKQYLADA  467

Query  506  W----KIFDQEEENRE--ERLKKWMDPKLESYYPIDYALSASLAVNCTADKSLSRPTIAE  559
          +  F  ++N E  E+LK W DP L++  P  D AL+  +A +C  +RP +  +
Sbjct  468  FVKLTDFAGDDNDEKIEKLHWADPILDNAVPWDIALNFVEVARSCVDADDPARPNMKD  527

Query  560  IVLSLSLLTQPS  571
          +  LS  L + S
Sbjct  528  VTFKLSKLESS  539

```



>ref|XP_002277331.1|  PREDICTED: hypothetical protein [Vitis vinifera]
Length=638

GENE ID: 100258108 LOC100258108 | hypothetical protein LOC100258108
[Vitis vinifera]

Score = 280 bits (716), Expect = 4e-73, Method: Compositional matrix adjust.

Identities = 188/628 (29%), Positives = 313/628 (49%), Gaps = 94/628 (14%)

Query	17	LVIMLFSTNIVAQSQOD-----NRTN-FSCPSDSPSCETYVTYIAQSPNFL	62
		+V++L VAQ+QQ N TN F C + P SC +Y+T+ + P++	
Sbjct	1	MVLLLLVWISVAQSQSYVNNHQLDCDNNFNETNGFQC--NGPRSCHSYLTFRSAPPSYD	58
Query	63	SLTNISNIFDTPSLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGD	122
		S +I+ + ++ P IA + + +D + KD VL+VPV C C+G+ N +Y +	
Sbjct	59	SPPSIAYLLNSEPAQIATINEVSDVD-TISKDTVLIVPVNCSGSGDFYQHNTTTLKSAS	117
Query	123	SFYF-VATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVPFLFCKCPSKNQLDKEIKYLI	181
		YF +A +Y+ LT +A+ NP N L +G+ + PL C CP+ NQ YL+	
Sbjct	118	ETYFSLANNYTGGLTTCQALKAQNPYDYRN-LSVGLHLQVPLMCACPTANQTAAGFNYLL	176
Query	182	TYVWKPGDNVSLVSDKFGASP-EDIMSENNYQGNFTAANNLPVLIPVTRLPVLARS----	236
		+Y+ GD + ++ FG + I N P+L+P+ P ++	
Sbjct	177	SYLVTWGDITDSIAKIFGVDDVQSIYDANRLSSTSIVYFPFTPILVPLKNPPSKIQTTVSS	236
Query	237	-----PSDGRKGIRLPVIGISLGCTLLVLVLAVLLVYVYCLKMKT-----	278
		PS G + V IG +G LLVL+++ +++ + + +	
Sbjct	237	PPAPSPETPMVPSGGGNSSSKKWVFIGAGIGAALLVLLISSGMMFCFRRRRQSGQDKPV	296
Query	279	-----LNRSSASSAETADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYK	330
		L++S + + L G+ + T+Y+ + + +A E +I SVY+	
Sbjct	297	LDLGEATKLSKLENKTSMSISLEGIRIEMESLTVYKYEELQKAAGYFGEANRIKGSVYR	356
Query	331	ANIEGKVLAVKRFKEDVTEELKILQKVNHGNNLVKLMGVSSDNDGNCFFVVEYAENGSLDE	390
		A+ +G A+K K DV+EE+ IL+++NH +++L G + GN ++VVEYAENG+L +	
Sbjct	357	ASFKGDDAAIKMMKGDVSEINILKQINHSKVIRLSGFCI-HAGNTYLVVEYAENGALRD	415
Query	391	WLFS--KSCSDTNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDS	448
		WL ++CS +L W QR+ +A D A L Y+H P +H+++ SNILLD	
Sbjct	416	WLHGDGTCS-----TLGWKQRVQIAYDAADALNYLHNFISSPCIHKNLKSINLLDG	468
Query	449	NFKAKIANFSMARTFTNP-----MMPKIDVFAFGVV	479
		N + K+ NF +AR N + PK+D+FAFGVV	
Sbjct	469	NMRGKVTFNFGLARLGNEEGDGGGLQLTRHVVGQTGYMAPEYVENGVTPKLDIFAFGVV	528
Query	480	LIELLTGRKAMTT--KENGEVVMWKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYAL	537
		+ELLTG++A + KE GE++ + I ++ Q +N ++L+ ++DP L YP D A	
Sbjct	529	ILELLTGKEAAPSQKKEGGELLSV--SINEVL-QGDNVVRDKLRGFIIDPCLAHEYFPDLAF	585
Query	538	SLASLAVNCTADKSLSRPTIAEIVLSLS 565	
		S+A LA +C A +RPT+++I + LS	
Sbjct	586	SMAQLAKSCVAHDNLNARPTMSDIFVILS 613	

>ref|XP_002974494.1|  hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii]
>gb|EFJ24716.1|  hypothetical protein SELMODRAFT_11327 [Selaginella moellendorffii]
Length=539

GENE ID: 9657733 SELMODRAFT_11327 | hypothetical protein
[Selaginella moellendorffii]

Score = 279 bits (714), Expect = 7e-73, Method: Compositional matrix adjust.
Identities = 189/552 (34%), Positives = 294/552 (53%), Gaps = 31/552 (5%)

Query	38	FSCPSDSPSCETYVTYIAQSPNFLSLTNISNIFDTPSLSIARASNLEPMDDKLVKDQVL	97
		+SC S+S SC+Y Y A + +L++ F S +A AS + LV DQVL	
Sbjct	1	YSCVSNST-SCQAYAAAYRALQGD--TLQSVGLRFRLSVEQLAEASQI-AQSATLVDPQVL	56
Query	98	LVPVTCGCTGNRSFANISYEINQGDSEFYFVATTSYENLTNWRVMDLNPVLSPNKLPIGI	157
		L+P+ C C RS N +Y I GD+ Y V+ ++ LT ++AV NP+ P L G	
Sbjct	57	LIPLNCSCASGRSQFNATYIIQSGDTLYLVSNGTFFQGLTTYQAVERANPLAVPTNLQPGD	116
Query	158	QVVPFLFCKCPSKNQLDKEIKYLIYVWKPGDNVSLVSDKFGASPEDIMSENNYQGNFTA	217
		+VFP+ C CPS Q+ + L+TY PG+ + ++ + S +S+N + T	
Sbjct	117	SIVFPIRCACFPSSAQVAGVTSLVYTSIWPGELDGIARAWNVSRTLASDNTVSGSATL	176
Query	218	ANNLPVLIPVTRLPVLARSPSDGRKGIRLPVIGISLGCTLLVLVLAVLLVYVYCLKMK	277
		+ P + S + +GI++ C VL++ + LV Y + +	
Sbjct	177	SPAAPPANNPPNNSPSPDSSSSSGSNTGM--YVGIACVAAVLLVVLALVIFYRRRPR	234
Query	278	TLNRSSASSAETADK-----LLSGVSGYV--SKPTMYETDAIMEATMNLSEQCKIGESV	328
		+ ++S AE + + LL+G+ G V +P ++ + +AT N S I SV	
Sbjct	235	KVTKASSYAEPSKEQPSPHAPLLAGMHGLVDSERPVPVFSYEELCDATNNFSASHLIQGSV	294
Query	329	YKANIEGKVLAVKRFKEDVT-EELKILQKVNHGNNLVKLMGVSSDNDGNCFFVVEYAENG	387
		Y+ + +++A+K K T +ELKIL KV+H NLVKL+G+ S +D F+VVEYA+NGS	
Sbjct	295	YRGILRQLVAIKEMKGGTTSQELKILCKVHNSNLVLIGICSGDD-KLFLVVEYADNGS	353
Query	388	LDEWLFKSCSDTNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLD	447
		L SC A+ W R+ +A+DVA GL+Y+H++ P VH+D+ SSNILLD	
Sbjct	354	L-----SSCLHNRTPAATAIWNTRLQVAMDVATGLEYIHDTKPSFVHKDVKSSNILLD	407
Query	448	SNFKAKIANFSMARTFTNP--MMPKIDVFAFGVVLIELLTGRKAMTTKENGEVVMWKDI	505
		+N +AK+ANF MAR + + K+DV+AFGVVL+EL TGR+A+ + G D	
Sbjct	408	ANLRKAVANFGMARLYLTHGFTTKVDVYAFGVVLELFTGREAILSTGTGSEKQYILADA	467
Query	506	W----KIFDQEEENRE--ERLKKWMDPKLESYYPIDYALSASLAVNCTADKSLSRPTIAE	559
		+ F ++N E E+LK W DP L++ P D AL+ +A +C +RP +	
Sbjct	468	FVKLTGDFAGDDNDEKIEKLKHWDPILDNAVPWDIALNFVEVARSCVDADDPARPNTKD	527
Query	560	IVLSLSLLTQPS 571	
		+ LS L + S	
Sbjct	528	VTFKLSKLLLESS 539	

>emb|CB117583.3| unnamed protein product [Vitis vinifera]
Length=1305

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 277 bits (709), Expect = 3e-72, Method: Compositional matrix adjust.
Identities = 171/565 (30%), Positives = 298/565 (52%), Gaps = 56/565 (9%)

```

Query 47      SCETYVTYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCT 106
+C+TY+ + ++SP + ++++IS++ + P +A+ +++ +V+ VPV C C+
Sbjct 719    TCQTYLIFRSESP-YNNVSSISDLLASDPSQLAQINSVTETATFDTNKEVI-VPVNCSCS 776

Query 107     GNRSFANISYEINQGDSEFYFVATTSYENLTNWRVMDLNPVLSFNKLPIGIQVVFPLFCK 166
GN S N SY + GD ++A +++ L+ +A+++ NP +S L G + PL C
Sbjct 777     GNYSQNTSYVVKNGDYPLWIANNTFQGLSTCQALLNQNPVSATNLNPGTSITVPLRCA 836

Query 167     CP SKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNGQNFTAANNLPVLIP 226
CP+K Q D +KYL++Y+ GD VS +S +FG E + N + T +LIP
Sbjct 837     CPTKQSDAGVYKLYMSYLVAYGDTVSAISGRFGVDTERTELEANESEQDTINPFTTLLIP 896

Query 227     VTRLPLVARSPSDGRKGIRLPVIIGISLGCTLLVLVLAVLLVYV-YCLKMKTINRSASS 285
+ P +++ I+ V + + + ++L+ ++V+ + K K N +
Sbjct 897     LQNPSSSSQT-----IKTWVYVIVGVAAGVLLFFGYVIFVKFFRKTKKKNDQIAV 948

Query 286     AET-----ADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIE 334
+E+ + +S +Y+ + + AT N S C I SVY+ I+
Sbjct 949     SESFKPLEKPLKVEEHEFFESISSMAQSVKVKFEELQSATDNFSPSCLIKGSVYRGTIK 1008

Query 335     GKVLAVKRFKEDVTEELKILQKVNHGNNLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFS 394
G + A+K+ +V+ E+ +L K+NH N+++L G+ NDG+ ++V+EYA NGSL +W++
Sbjct 1009    GDLAATKKMDGNNSEIALLSKINHFNIVRLSGICF-NDGHWYLVHEYAVNGSLSDWIYY 1067

Query 395     KSCSDTSNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKI 454
+ N R L W QRI +A+DVA GL Y+H H P +H+D+ S+N+LLD +F+AKI
Sbjct 1068    NN-----NDRRLFLVWTQRIQIALDVATGLNYLHIHVSYSYIHKDKMSNNVLLDGDGRAKI 1122

Query 455     ANFSMARTFTNP-----MMP-----KIDVFAFGVVLIELLTGRK 488
ANF AR+ M P K+DV+AFGV+++E+ TG K
Sbjct 1123    ANFDQARSAEQGEGQFALTRHIVGTGKGYMAPEYLENGLISTKLDVYAFGVLMLEIFTG-K 1181

Query 489     AMTTKENGVEVMLWKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYALSASLAVNCTA 548
+ GE + L + + + E++ +E+L ++DP L+ YP + A+ + L +C
Sbjct 1182    EVAALYGGESIHLSSEVLA AVL-HEDDGKEKLGDFIDPSLDGNYPELAIFMIRLIDSCLT 1240

Query 549     DKSLSRPTIAEIVLSLSLLTQPSA 573
RP + EIV SLS + S A
Sbjct 1241    KAPAGRPDMDEIVQSLSRILASSQA 1265

```

Score = 273 bits (698), Expect = 6e-71, Method: Compositional matrix adjust.
Identities = 177/557 (31%), Positives = 297/557 (53%), Gaps = 56/557 (10%)

```

Query 47      SCETYVTYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCT 106
SC+ ++ + ++ P + ++++IS++ + P +A+ ++++ K +V+ VPV C C+
Sbjct 74      SCQAFLIFRSEPP-YNDVSSISDLLGSDPSQLAQINSVDETATFETKKEVI-VPVNCSCS 131

Query 107     GNRSFANISYEINQGDSEFYFVATTSYENLTNWRVMDLNPVLSFNKLPIGIQVVFPLFCK 166
G S AN SY + GD++ +A ++E L+ +A+ L N + G ++ PL C
Sbjct 132     GEFSQNTSYVVVQHGDTYLLIANNTFEGSLTCQALRSQRTSLTTN-IYTGTKLTVPLRCA 190

Query 167     CP SKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNG-QNFTAANNLPVLI 225
CP+KNQ D +KYL++Y+ GD VS +S +FG + N QN P +
Sbjct 191     CPTKNQSDVGKLYMSYLVASGDYVSSISVRFVGVDGMTLEANESEQN-----PNII 243

Query 226     FVTRLPV-LARSPSDGRKGIRLPVIIGISLGCTLLVLVLAVLLVYVYCLKMKTINRSAS 284
P T L + L PS + + V+G+ G L+L +V+ + K + A
Sbjct 244     EFTTLLPLQLNPSSSQTIKTWVYVVVGVAAGVLLVLFSGSVIFFKFFRKTTRKTDPIAI 303

Query 285     S-----AETADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIE 334
S E + L +S +Y+ + + AT N S C+I SVY+ I+
Sbjct 304     SESFEACEKPLKEQHEFLESISIAQSLKVYKFEELQSATDNFSPNCRIKGSVYRGTIK 363

Query 335     GKVLAVKRFKEDVTEELKILQKVNHGNNLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFS 394
G + A+K+ +V+ E+ +L K+NH N+++L G+ NDG+ ++V+EYA NG L +W+++
Sbjct 364     GDLAATKKMDGEVSEIALLNKINHFNIVRLSGICF-NDGHWYLVHEYAVNGPLTDWIYN 422

Query 395     KSCSDTSNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKI 454
+ +SR L W QRI +A+DVA GL Y+H + P VH+DI S N+LLDS+F+AKI
Sbjct 423     ----NNDSDRF-LVWMQRIQIALDVATGLNYLHSYTSPPYVHKDIKSGNVLLSDDFRAKI 477

Query 455     ANFSMARTFTNP-----MMP-----KIDVFAFGVVLIELLTGRK 488
ANF +AR+ M P K+DV+AFGV+++E+LTG++
Sbjct 478     ANFGLARSAEQGEGQFALTRHIIIGTRGYMAPEYLENGLVSTKLDVYAFGVLMLEMLTGKE 537

Query 489     AMTTKENGVEVMLWKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYALSASLAVNCTA 548
E GE + L D+ E + +E+L+ ++DP L YP++ A+ + L +C
Sbjct 538     VAALYE-GENMHL-PDVLVAVLHEGDGKEKLRNFIDPSLSGNYPLELAIVMIRLIDSCCLK 595

Query 549     DKSLSRPTIAEIVLSLS 565
SRP + EIV +LS
Sbjct 596     KSPASRPDMVEIVQALS 612

```

>ref|XP_002510333.1| serine-threonine protein kinase, plant-type, putative [Ricin
communis]

gb|EEF52520.1| serine-threonine protein kinase, plant-type, putative [Ricin
communis]
Length=637

GENE ID: 8260932 RCOM 1593420 | serine-threonine protein kinase, plant-type,
putative [Ricin communis]

Score = 276 bits (707), Expect = 5e-72, Method: Compositional matrix adjust.
Identities = 168/555 (30%), Positives = 295/555 (53%), Gaps = 49/555 (8%)

```

Query 47      SCETYVTYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCT 106
+C+ ++ + ++ P + S IS + S +AR +N+ + + + +V+ VPV+C C
Sbjct 54      TCQAFLIFRSRPP-YDSAPTISALTSASQEELARFNNVTGLSEFPLNKEVI-VPVSCSCL 111

Query 107     GNRSFANISYEINQGDSEFYFVATTSYENLTNWRVMDLNPVLSFNKLPIGIQVVFPLFCK 166
G AN S+++ S++ +A+ +YE L+ ++ N + L +G ++ PL C
Sbjct 112     GQYYQANTSFQVASDHSYFTIASQTYEGLSTCASLKKAN-IYGEFDLALGAELQVPLRCA 170

Query 167     CP SKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNGQNFTAANNLPVLIP 226

```

```

Sbjct 171 CP+ +Q+ E KYL+T+ D+++ ++++F S E I+ N ++ T + +LIP 230
          CPTASQVRNETKYLTLTPISESDHIAAIAERFNVSKESIIDANGLRESPTIYPDTTILIP
Query 227 VTRLPEVLAR-----SPSDGRKGGIRLPVIIGISLGCTLLVLVLAVLLVYV 271
          +T P ++ SP D R+ +L +GI+ C+LLVL + V++++
Sbjct 231 LTTEPSNSQTTIHENPTEVSPPLASPPDNRRSRKRKLYEKGITAACSLLVLSIIVVILFL 290
          + + + + L ++ + + + +AT N S + I S+Y
Query 272 YCLKMKTLNRSASSAETADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKA 331
          + + + + L ++ + + + +AT N S + I S+Y
Sbjct 291 LRKDRRHKFPFENRRREQEDLRLEIASVEQVLKVFGLVEVKKATDNFSSKHIKGSILYWG 350
          + + + + L ++ + + + +AT N S + I S+Y
Query 332 NIEGKVLAVKRFKEDVTEELKILQKVNHNGLVKLMGVSSDNDGNCVFVVEYAENGSLDEW 391
          G++LA+K+ DV++E+ IL+++NH NL+KL GV +N G ++ +EY +NGSL EW
Sbjct 351 EFGQILAIKKMNRDVSKEVNIILKRINHFNLIKHLHGVC-ENLGCFFYLFFEYMKNGSLQEW 409
          + + + + L ++ + + + +AT N S + I S+Y
Query 392 LFSKSCSDTNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFK 451
          L + D +W QRI +A+D+A GL Y+H P VH+DITS +ILLD+N +
Sbjct 410 LSRERFEDVG-----SWNQRIQIALDIANGLFYLHSFTEPACVHKDITSGHILLDNNLR 463
          + + + + L ++ + + + +AT N S + I S+Y
Query 452 AKIANFSMARTFTNPM-----PKIDVFAFGVVLIELLTGRKA 489
          AKIANFS+AR N ++ PKIDV+AFG+VL+EL+TG+ A
Sbjct 464 AKIANFSLARAAANAVLTKHIEGTRGYMAPEYVQAGQVTPKIDVYAFGIVLLELITGKDA 523
          + + + + L ++ + + + +AT N S + I S+Y
Query 490 MTTKENGEVVMLWKDIWKIFDQENREERLKKWMDPKLESYYPIDYALSLASLAVNCTAD 549
          + ++ G+ +L K I+ + ++ EN E L +DP AL LA +++ C
Sbjct 524 VFMRD-GKETLLSKAIFSVMEK-ENAEAEALAFVIDPSFTGGRQSKLALRLARVSLACLTQ 581
          + + + + L ++ + + + +AT N S + I S+Y
Query 550 KLSLRPTIAEIVLSL 564
          RP++ E+V +L
Sbjct 582 VPARRPSMGEVVSSTL 596
          + + + + L ++ + + + +AT N S + I S+Y

```

>dbj|BAI79276.1| LysM type receptor kinase [Lotus japonicus]
Length=633

Score = 276 bits (705), Expect = 7e-72, Method: Compositional matrix adjust.
Identities = 193/612 (31%), Positives = 315/612 (51%), Gaps = 93/612 (15%)

```

Query 38 FSCPSDSP-PSCEYTVTYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQV 96
          ++C S ++C+ Y+T+ Q P + S+ IS + + +A ++ + + + +
Sbjct 49 YTCNGGSANHTCQAYLTFRTQ-PIYNSVYTISTLLSSDARHLAETMSVS-QNTTFETNKL 106
          + + + + L ++ + + + +AT N S + I S+Y
Query 97 LLVPVTCGCTGNRSFANISYEINQGDSFYFVATTSYENLTNWRVMDLNPVLSPNKLPFG 156
          ++VFPV C C G AN SY D+ + +A ++E LT +A+M N +P L +G
Sbjct 107 VIVFPVQSCCAGEYYQANTSYAFQNTDTPFSIANNTFEGLTTCQALMHENH--NPGHLYLG 164
          + + + + L ++ + + + +AT N S + I S+Y
Query 157 IQVVFPLFCCKPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYGNFT 216
          ++ PL C CP+KNQ +K IKYL++Y+ GD+VS++S+KFG S + + N+ + T
Sbjct 165 RELTVPLRCACPTKNQTEKGIKYLSSYLVNWGDSVSVISEKFGVSCNNTLEANSL--SLT 222
          + + + + L ++ + + + +AT N S + I S+Y
Query 217 AANNLP---VLIPVTRLPLVARS-----PSDGRKGGIRLPVIIGISLG 256
          A P +L+P+ P +++ + L V++G G
Sbjct 223 KAKIYPTTLLVPLHDKPSNSQTILQSQPSSTSSPPSSSTHQSSNKTWLYVVVG---G 279
          + + + + L ++ + + + +AT N S + I S+Y
Query 257 CTLLVLVLAVLLVYVY-----CLKMKTNLRSASSAETADKLLSG-----VSGYVS 301
          L+++ AV+ Y L T++ S + + ++ G + G
Sbjct 280 VFALIVLTAVIFCIHYHKGRKKDDSLSQLTVSESFENQQLGKEMKKGDGKLSEFIHGIAQ 339
          + + + + L ++ + + + +AT N S + I S+Y
Query 302 KPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHN 361
          +Y + I AT NL+ I SVY+ + G ++A+K+ + DV++E++IL KVNH N
Sbjct 340 SFKVYSFEETQRATNNLNSSSLIKGSVYRGVMNGDLVAIKTEGDVSKETIILNKVNHSN 399
          + + + + L ++ + + + +AT N S + I S+Y
Query 362 LVKLMGVSSDNDGNCVFVVEYAENGSLDEWLFKSCSDTNSRASLTWCQRISMAVDVAM 421
          ++L GVS N+G ++VVEYA NG L EW+F L+W QRI +A+DVA+
Sbjct 400 VIRLSGVSF-NEGQWYLVVEYAANGPLSEWIFFGKF-----LSWTQRIQIALDVAI 449
          + + + + L ++ + + + +AT N S + I S+Y
Query 422 GLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNP----- 466
          GL Y+H P +H+D+ SSNILLDS+F+AKIAN S+AR+
Sbjct 450 GLDYLSHFTSPPHIHKDLKSSNILLDSDFRAKIANLSLARSVKGVEDDQFLATRNIVGT 509
          + + + + L ++ + + + +AT N S + I S+Y
Query 467 ---MMP-----KIDVFAFGVVLIELLTGRK--AMTTKENGEVVMLWKDIWKIFDQ 511
          M P K+DV+AFGV+++E+LTG++ A+ ++N K++ +
Sbjct 510 RGYMAPEYLENGLVSTKLDVYAFGLMLEILTGEKVAAILAEDNN-----KNLSGVLSA 563
          + + + + L ++ + + + +AT N S + I S+Y
Query 512 EENREERLKKWMDPKLESYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSLSLLTQPS 571
          EERLK++MDP L+S YP + A+ + + V C SRP++ EIV +LS T S
Sbjct 564 VLG-EERLKEFMDPSLQSNYPFELAMFVFEIIVGCEIKDPASRPMSQEIIVPTLS-RTMNS 621
          + + + + L ++ + + + +AT N S + I S+Y
Query 572 PATLERSLTSSG 583
          + E S+ SG
Sbjct 622 SLSWEMSVNISG 633
          + + + + L ++ + + + +AT N S + I S+Y

```

>dbj|BAI79286.1| LysM type receptor kinase [Lotus japonicus]
Length=633

Score = 276 bits (705), Expect = 8e-72, Method: Compositional matrix adjust.
Identities = 192/612 (31%), Positives = 315/612 (51%), Gaps = 93/612 (15%)

```

Query 38 FSCPSDSP-PSCEYTVTYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQV 96
          ++C S ++C+ Y+T+ Q P + S+ IS + + +A ++ + + + +
Sbjct 49 YTCNGGSANHTCQAYLTFRTQ-PIYNSVYTISTLLSSDARHLAETMSVS-QNTTFETNKL 106
          + + + + L ++ + + + +AT N S + I S+Y
Query 97 LLVPVTCGCTGNRSFANISYEINQGDSFYFVATTSYENLTNWRVMDLNPVLSPNKLPFG 156
          ++VFPV C C G AN SY D+ + +A ++E LT +A+M N +P L +G
Sbjct 107 VIVFPVQSCCAGEYYQANTSYAFQNTDTPFSIANNTFEGLTTCQALMHENH--NPGHLYLG 164
          + + + + L ++ + + + +AT N S + I S+Y
Query 157 IQVVFPLFCCKPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYGNFT 216
          ++ PL C CP+KNQ +K IKYL++Y+ GD+VS++S+KFG S + + N+ + T
Sbjct 165 RELTVPLRCACPTKNQTEKGIKYLSSYLVNWGDSISVISEKFGVSCNNTLEANSL--SLT 222
          + + + + L ++ + + + +AT N S + I S+Y
Query 217 AANNLP---VLIPVTRLPLVARS-----PSDGRKGGIRLPVIIGISLG 256
          A P +L+P+ P +++ + L V++G G
Sbjct 223 KAKIYPTTLLVPLHDKPSNSQTILQSQPSSTSSPPSSSTHQSSNKTWLYVVVG---G 279
          + + + + L ++ + + + +AT N S + I S+Y
Query 257 CTLLVLVLAVLLVYVY-----CLKMKTNLRSASSAETADKLLSG-----VSGYVS 301
          L+++ AV+ Y L T++ S + + ++ G + G
Sbjct 280 VFALIVLTAVIFCIHYHKGRKKDDSLSQLTVSESFENQQLGKEMKKGDGKLSEFIHGIAQ 339
          + + + + L ++ + + + +AT N S + I S+Y

```

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Query 302 KPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHG 361
          +Y + I AT NL+ I SVY+ + G ++A+K+ + DV++E++IL KVNH N
Sbjct 340 SFKVYSFEETQRAATNNLNSSSLIKGSVYRGVMNGDLVAIKKTEGDVSKETQILNKVNHSN 399

Query 362 LVKLMGVSSDNDGNCFFVVEYAENGLDEWLFKSKSDTNSRASLTWCQRISMAVDVAM 421
          ++L GVS N+G ++VVEYA NG L EW+F L+W QRI +A+DVA+
Sbjct 400 VIRLSGVVSF-NEGQWYLVVEYAANGPLSEWIFFGKF-----LSWTQRIQIALDVAI 449

Query 422 GLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNP----- 466
          GL Y+H P +H+D+ SSNILLDS+F+AKIAN S+AR+
Sbjct 450 GLDYLSHFTSPPHIHKDLKSSNILLSDSDFRAKIANLSLARSVKGVEDDQFLATRNIVGT 509

Query 467 ---MMP-----KIDVFAFGVVLIELLTGRK--AMTTKENGVEVVLWKDIWKIFDQ 511
          M P K+DV+AFGV+++E+LTG++ A+ ++N K++ +
Sbjct 510 RGYMAPEYLENGLVSTKLDVYAFGVLMLEILTGEKVAAILAEDNN-----KNLSGVLSA 563

Query 512 EENREERLKKWMDPKLESYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSLSLLTQPS 571
          EERLK++MDP L+S YP + A+ + + V C SRP++ EIV +LS T S
Sbjct 564 VLG-EERLKEFMDPSLQSNYPFELAMFVFEIIVGCEIKDPASRPSMQEIVPTLS-RTMNS 621

Query 572 PATLERSLTSSG 583
          + E S+ SG
Sbjct 622 SLWEMSVNISG 633

```

>gb|ABQ59612.1| LYK4 [Glycine max]
Length=633

Score = 270 bits (689), Expect = 5e-70, Method: Compositional matrix adjust.
Identities = 191/646 (29%), Positives = 329/646 (50%), Gaps = 90/646 (13%)

```

Query 4 FFPFLPLHSQILCLVIMLFSTNIVAQSQQDNRTNFSCP-----SDSPSCET 50
          FFE+P+ I L+I FS I+ Q +CP + + + SC++
Sbjct 3 LFFPIPI--IIFTLIHNFSL-ILGQQPYIGLGTVACPRRGKNKSIRGYTCNGANHSCQS 59

Query 51 YVTYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRS 110
          Y+T+ +Q P + S+ IS + + P +A+ +++ M+D +++++VVPV C C G
Sbjct 60 YLTFRSQ-PIYNSVKTISTLLGSDPSQLAKINSVS-MNDTFETNKLVIIVPNCSCAGEYY 117

Query 111 FANISYEINQGDSFYFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSK 170
          N SYE + +++ +A ++E LT +A+ + N +P + G +++ PL C CP+K
Sbjct 118 QTNTSYEFHSETYFLIANNTFEGLTTCQALENQNH--NPANIYPGRRLVLPLRCACPTK 175

Query 171 NQLDKEIKYLITYVWVKPGDNVSLVSDKFGASPEDIMSENNYGNFTAANNLP---VLIPV 227
          NQ +K I+YL++Y+ GD+VS +S+KEG + + N T A P +L+P+
Sbjct 176 NQTEKGIRYLLSYLVNWGDSVSFISEKFGVNFMTTLEANTL--TLTQATYIPFTTILVPL 233

Query 228 TRLPVLARSPSDGRKGGIRLPVIIGISLGCTLL-----VLVLAVLLVYVYCLMK 277
          P +++ S R+ P S T+ + + + +VL ++ + +
Sbjct 234 HDKPSSQTVSPTRTRTPPPSPSSDHSSNKTWVYVVVGVVGAIALISVLCVIFFFTRYR 293

Query 278 TLNRSASSA-----ETADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQ 321
          + S + +KL +SG +Y + + AT N S
Sbjct 294 KNKKDDSVVVGSKSFEAIEEKPEVKVNEKLSEIISGIAQSFVYNFEELQRAITDNFSPS 353

Query 322 CKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGKLVKLMGVSSDNDGNCFFVVE 381
          I SVY+ I G + A+KR + DV++E++IL K+NH N++L GVS ++G ++VVE
Sbjct 354 SWIKGSVYRGVINGDLAAIKRIEGDVSKEIEILNKINHNSVIRLSGVVSF-HEGGWYLVVE 412

Query 382 YAENGLDEWLFKSKSDTNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITS 441
          YA NG L EW++ + + L+W QR+ +A+DVA GL Y+H P +H+DI S
Sbjct 413 YAANGDLSEWYIFHNVNG-----KFLSWTQRMQIALDVATGLDYLSHFTSPPHIHKDINS 467

Query 442 SNILLDSNFKAKIANFSMARTFTNP-----MMP-----KIDVFA 475
          SNILLD +F+ K+ N S+AR M P K+DV+A
Sbjct 468 SNILLDGDGRGKVTNLSLARCLEGGDDQLPATRHIVGTRGYMAPEYLENGLVSTKLDVYA 527

Query 476 FGVVLIELLTGRK--AMTTKENGVEVVLWKDIWKIFDQENREERLKKWMDPKLESYYPI 533
          FGV+++E++TG++ A+ T++ ++ + I EE+ +E LK+++DP L P+
Sbjct 528 FGVLMLEMTVGKEVAAILTEDETKLSHVLSGILG----EESGKEMLKEFVDP SLGENCPL 583

Query 534 DYALSLASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATLERSL 579
          + A+ + + NC SRP++ EIV S+S T S + ERS+
Sbjct 584 ELAMFVIEMIDNCIKTDPASRPSVHEIVQSMS-RTLKSSLSWERSM 628

```

>emb|CB140796.3| unnamed protein product [Vitis vinifera]
Length=680

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 269 bits (687), Expect = 1e-69, Method: Compositional matrix adjust.
Identities = 170/518 (32%), Positives = 279/518 (53%), Gaps = 45/518 (8%)

```

Query 70 IFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSFYF-VA 128
          + +++P IA + + + + K+ KD VL+VPV C C+G+ N SY + YF +A
Sbjct 151 LLNSNPDIATINQISDVN-KIPKDTVLIVFPVNCSCSGHFYQYNASYTLKYDFENYFTLA 209

Query 129 TTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYVWVKPG 188
          +Y+ LT +A+ NP N L +G+ ++ PL C CP+ NQ YL+TY+ G
Sbjct 210 NNITYQGLTTCCQALKAHNPYYRNL-SVGMDDLVLPLMCACPTANQTAAGFNYLLTYLVTWG 268

Query 189 DNVSLVSDKFGASPEDIMSENNYGNFTAANNLP-----PVLIPVTRLPVLARSP-- 237
          D +S ++D FG +DI Q+ AN+L P+L+P+ P ++
Sbjct 269 DYISSIADTFGV--DDI-----QSIFDANSLSSDLIFPFTPILVPLKNPPTRIQTTL 319

Query 238 -----SDGRKGGIRLPVIIGISLGCTLLVLVLAVLLVYVYCLMKTLNRSASSAE 287
          + G + V +G+ +G TLVLV++ ++ C K + + + +
Sbjct 320 PPPPKSPVVPNGGADSSKKWVYVGVGIGATLLVLMLPMSGIIL--CTKKPSYSMENNISL 377

Query 288 TADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDV 347
          + G+ V T+Y+ + + +A E +I VY+ I+G A+K K DV
Sbjct 378 SVSS--GGIHHAVESLTVYKYEELQKAAGFFGEANRIKGCVYRGLIKGDDAAIKMMKGDV 435

Query 348 TEELKILQKVNHGKLVKLMGVSSDNDGNCFFVVEYAENGLDEWLFKSKSDTNSRASL 407

```

```

Sbjct  436  +EE+ IL+ +NH N+++L G      + GN ++VVEYAENGL +WL      ++L
      SEENILKLNHNSVIRLSGFCV-HKGN TYLVVEYAENGLSDWLHGDG-----RIGSTL  489
Query  408  TWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPM  467
      W QR+ +A DVA L Y+H P +H+++ SSNILLD N + K+ANF +AR N
Sbjct  490  GWKQRVQIACDVANALNYLHNFTNPPCIHKNLKSSNILLDGNMRGKVANFGLARRLENEE  549
Query  468  MPKIDVFAFGVVLELLTGRKAMTTKENGVEVVMWKDIWKIFDQEEENREERLKKWMDPKL  527
      ++D FAFGVV++ELLTG++A + +N E L + ++ + ++ R +L+ ++DP L
Sbjct  550  GGELDAFAFGVVILELLTGKEAAPS-QNKEGRGLCVSVNEVLEGDDVR-HKLRGFI DPCL  607
Query  528  ESYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSLS  565
      YP D A ++A LA +C A +RPT+ +I++ LS
Sbjct  608  THDYPFDLAFTMAQLAKSCIAHDLNARPTMFDILILIS  645


```

Score = 78.6 bits (192), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 43/99 (43%), Positives = 66/99 (66%), Gaps = 5/99 (5%)

```

Query  469  PKIDVFAFGVVLELLTGRKAMTT--KENGEVVMWKDIWKIFDQEEENREERLKKWMDPK  526
      PK+D+FAFGVV++ELLTG++A + KE GE +L I ++ Q +N ++L+ ++DP
Sbjct  30  PKLDIFAFGVVILELLTGKEAAPSQKKEGGE--LLSVSINEVL-QGDNVDRDKLGRGFI DP  86
Query  527  LESYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSLS  565
      L YP D A S+A LA +C A +RPT+++I + LS
Sbjct  87  LAHEYPFDLAFSMAQLAKSCVAHDLNARPTMSDIFVILS  125

```

>ref|XP_002269442.1|  PREDICTED: hypothetical protein [Vitis vinifera]
Length=632


GENE ID: 100264999 LOC100264999 | hypothetical protein LOC100264999
[Vitis vinifera]

Score = 268 bits (685), Expect = 1e-69, Method: Compositional matrix adjust.
Identities = 170/583 (29%), Positives = 296/583 (50%), Gaps = 69/583 (11%)

```

Query  47  SCETYVITYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCT  106
      +C+TY+ + ++SP + +++IS++ + P +A+ +++ ++ ++VFP C C+
Sbjct  54  TCQTYLIFRSESP-YNNVSSISDLLASDPQLAQINSVTETA-TFDTNKEVIVFPVNCSCS  111
Query  107  GNRSFANISYEINQGDSEFYFVATTSYENLTNWRRAVMDLNPVLSFNKLPFIGIQVFPFLFCK  166
      GN S N SY + GD ++A +++ L+ +A+++ NP +S L G + PL C
Sbjct  112  GNYSQTNSTSVVKNGDYPLWIANNTFQGLSTCQALLNQNPVSATNLNPGTSTITVPLRCA  171
Query  167  CPSKNQLDKKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYGNFETAANNLPVLIP  226
      CP+K Q D +KYL++Y+ GD VS +S +FG E + N + T +LIP
Sbjct  172  CPTRAQSDAGVKYLMXYLVAYGDTVSAISGRFGVDTERTEANELSEQDITINPFTTLLIP  231
Query  227  VTRLPEVLARS-----PSDGRKGGIRLPVIGISLGCTLLVLVLAVL  267
      + P +++ +K + + V + +L+L +
Sbjct  232  LQNPPSSSQTI VPPPPPPPPPPSAVSSPSGSSKKTWVYVIVGVAAG---VVL LFFGYV  288
Query  268  LVVYVYCLMKMTLNRSAASAET-----ADKLLSGVSGYVSKPTMYETDAIMEATM  316
      + + K K N + +E+ + +S +Y+ + + AT
Sbjct  289  IFVKFFRKTKKKNDQIAVSESFKEKPLEKPLKVEEHEFFESISSMAQSVKVKFEELQSATD  348
Query  317  NLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNLVKLMGVSSDNDGNC  376
      N S C I SVY+ I+G + A+K+ +V+ E+ +L K+NH N+++L G+ NDG+
Sbjct  349  NFSPSCLIKGSVYRGTKGDLAAIKKMDGNVSNEIALLSKINHFNIRLSGICF-NDGHW  407
Query  377  FVVEYAENGLSDEWLFKSCSDTSNSRASITWCQRISMAVDVAMGLQYMHEHAYPRIVH  436
      ++V+EYA NGSL +W++ + N R L W QRI +A+DVA GL Y+H H P +H
Sbjct  408  YLVHEYAVNGSLSDWIYYNN-----NDRRLVWVTQRIQIALDVATGLNYLHIHVSPSYIH  462
Query  437  RDITSSNILLDSNFKAKIANFSMARTFTNP-----MMP-----K  470
      +D+ S+N+LLD +F+AKIANF AR+ M P K
Sbjct  463  KDMKSNNVLLDGDFAKIANFDFQARSAGQGEGFALTRHIVGTGKGYMAPEYLENGLISTK  522
Query  471  IDVFAFGVVLELLTGRKAMTTKENGVEVVMWKDIWKIFDQEEENREERLKKWMDPKLESY  530
      +DV+AFGV++E+ TG K + GE + L + + + E++ +E+L ++DP L+
Sbjct  523  LDVYAFGVLMLEIFTG-KEVAALYGGESIHLSEVLAAVL-HEDDGKEKLGDFIDPSLDGN  580
Query  531  YPIDYALSLASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSA  573
      YP + A+ + L +C RP + EIV SLS + S A
Sbjct  581  YPPELAIFMIRLIDSLTKAPAGRPDMDEIVQSLSRILASSQA  623

```

>ref|XP_002533279.1|  serine-threonine protein kinase, plant-type, putative [Ricinus communis]
gb|EEF29111.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]
Length=617

GENE ID: 8272991 RCOM_0411670 | serine-threonine protein kinase, plant-type,
putative [Ricinus communis]

Score = 265 bits (676), Expect = 2e-68, Method: Compositional matrix adjust.
Identities = 187/601 (31%), Positives = 315/601 (52%), Gaps = 78/601 (12%)

```


Query  22  FSTNIVAQSQQDNRTN----FSCPSDSPSPSCETYVITYIAQSPNFLSLTNISNIFDTSPLS  77
      +S N+V ++ T F + SC+T++ Y +Q P + ++++IS + + PL
Sbjct  25  YSGNLVMNCDNNDSTGPSAPFLYTCNGKESCKTFLLIYKSQPP-YHTVSSISKLTSSDPLE  83
Query  78  IARASNLEPMDDKLVDQVLLVPVTCGCTGNRSFANISYEI-NQGDSEFYFVATTSYENLT  136
      +A +N+ L ++ ++VP+ C C+ AN SY I + D+++ +A ++YE L+
Sbjct  84  LALINNISNFT-VLPTNKEVIVPIICSCSSQYQANTSYYIIPSIYDITYFSIAESTYEGLS  142
Query  137  NWRRAVMDLNPVLSFNKLPFIGIQVFPFLFCKCPSKNQLDKKEIKYLITYVWKPGDNVSLVSD  196
      ++M N S L +G+++ PL C CP+ NQ KYL+TY GD V VS+
Sbjct  143  TCNSLMRQNN-YSEFSLDVGMELRVPLRCACPTSNQSANGTKYLLTYSVSWGDKVRAVSE  201
Query  197  KFGASPEDIMSENNYGNFETAANNLPVLIPVTRLFPV-LARSPSDGRK-----  242
      +F AS L + NY FT + L P T + V L+ PS +
Sbjct  202  RFNASIDSV----NYANGFTKDDT--TLFPFTTILVPLSTEPSSFTIVHYPPPPYSPPF  255
Query  243  ---GGIR-----LPVIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSAASAETA  289

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      IR                +PVII +L  L +++L  L      L ++      + E
Sbjct 256 IPVPIRRSRKKIHVWVPIVIVSALPVVLFIVLL--LRNKKSHLGVQREKEGKNKEELP 313
Query 290 DKLKSGVSGVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTE 349
      D L V+      +Y + + AT + S ++ +SVY+ I G+VLA+K+ +DV+
Sbjct 314 DDFLDHVAHVLDGLKIYTFEELKVATEDFSTSNRLSDSVYRGVISGQVLAIKKMSKDVSN 373
Query 350 ELKILQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSKSCSDTNSRASLTW 409
      E+ +L+K+NH NL+ L + ++ G +++YE+ +NGSL +WL+ ++C + +W
Sbjct 374 EVTLLRKINHNFLNISLHA-ACEHHGVFYLMYEFMDNGSLRDWLYKRNCLEAQ-----SW 426
Query 410 CQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMART----- 462
      +RI +A+DVA GL Y+H P VH+DI+SSN+LL + +AKIANFS+AR+
Sbjct 427 NRRIQIALDVANGLHYLHNFTDPPYVHKDISSSNVLLSRHLRAKIANFSLARSAKAEHV 486
Query 463 -----FTNP-----MMPKIDVFAFGVVLELLTGRKAMTTKENGEEVVMWLK 503
      + P + P+ID++AFGVVL+EL+TG++A+ +E +V L +
Sbjct 487 NSSRLRALGSKGYLAPEFIDFGLVTPETIDIYAFGVVLELVLTGKEAVYMQEERKV-QLSE 545
Query 504 DIWKIFDQEEENREERLKKWMDPKLESYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLS 563
      I I ++E N E RL +DP L+S + ++ L + L++ C A + SRP++AEIV +
Sbjct 546 TIISIMEKE-NAEARLGCIVDPNLQSQHSMEVVLRMVKLSLACLAQEPESRPSMAEIVSA 604
Query 564 L 564
Sbjct 605 L 605

```

>ref|XP_002533278.1|  BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]
gb|EEF29110.1| BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]
Length=647


GENE ID: 8272990 RCOM 0411660 | BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative [Ricinus communis]

Score = 265 bits (676), Expect = 2e-68, Method: Compositional matrix adjust.
Identities = 181/601 (30%), Positives = 306/601 (50%), Gaps = 87/601 (14%)

```

Query 33 DNRNTEFCSPSDSPSCETYYVYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKL 92
      D+ +SC + SC+TY+T+ +Q P + ++T+IS + ++ P ++ A N
Sbjct 42 DSALGYSNGLNTSCQTYLTFRSQPP-YTNVTSISTLLNSDPSQLS-AINSVSETATFD 98
Query 93 KDQVLLVPVTCGCTGNRSFANISYEINQGDSEFYFVATTSYENLTNWRVMDLNPVLS 152
      +++++VPV C C+G+ AN SY + D +F+A +++ L+ +A+ D N + +
Sbjct 99 TNKLIVIVPVCSCSGDYQANTSYVVQAKDAPFFIANNTFQGLSTCQAINQNRRTQVDI 158
Query 153 LPIGIQVVFPLFCCKPSKNQLDKEIKYLITYVVKPGDNVSLVSDKFGASPEDIMSENNYG 212
      P I + PL C CP+KNQ D IKYL++Y+ GD VS VS KFG + + N
Sbjct 159 FPNEI-LHIPRCACPTKNQTDAGIKYLLSYLVWGTVSAVSVKFGNGTGRSLEANGLS 217
Query 213 -QNFTAANNLPVLIPVTRLPV-----LARSPSDGRKGGIRLPVIG 252
      Q T +LIP+ P +P++G + V++G
Sbjct 218 EQTPTIYFPTLLIPLNPPTSNTQISPPPPPPASSPPPPSTDTPNNGSSSKKVVVYLVG 277
Query 253 ISLGCTLLVLVLAVLLVYVYCL-----KMKTLNRSASSAETADKLL 293
      + G +V L ++ + Y L + + K+LN+ + E + L
Sbjct 278 VLAG---IVFTLGLVTIIFYALFRSRKRKPEPIIVSESFEAQEKS LNKLD--EESQDFL 332
Query 294 SGVSGVSKPTMYETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKI 353
      +S +Y+ + AT N S C I SVY+ I G A+K+ DV++E+++
Sbjct 333 DSISIIAQSIKIVYKFELEAATDNFSPSCWIKGSVYRGYISGDYAAIKVNGDVSKIEL 392
Query 354 LQKVNHNGLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSKSCSDTNSRASLTWCORI 413
      L KVNH NL++L GV G+ ++VVEYA NG+L +W++ ++N L+W QR+
Sbjct 393 LNKVNHNFLRLSGVCFSG-GHWYLVVEYAANGALSDWIYY-----SNNEGNFLSWTORV 446
Query 414 SMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNP----- 466
      +A+DVA GL Y+H P +H+DI SSN+L+DS+F+AKIAN +MAR+
Sbjct 447 QIALDVATGLNLYHSFTSPPHHKDIKSSNVLIDSDFRAKIANLAMARSTEGQDGEFALT 506
Query 467 -----MMP-----KIDVFAFGVVLELLTGRK--AMTTKENGEEVVMWLKDI 505
      M P K+DV+AFG+++E++TG++ A+ T+EN + + D+
Sbjct 507 RHIVGTGKGYMAPEYLENGLVSTKLDVYAFGILMLEMVTGKEVAALYTEENLNLSDIINDV 566
Query 506 WKIFDQEEENREERLKKWMDPKLESYYPIDYALSLASLAVN-CTADKSLSRPTIAEIVLS 564
      +E+ ++ LK+++DP +E +P + +L + ++ C RP + EI SL
Sbjct 567 LS----KEDGQQLKQVDPDSMEENFPSEISLFMMVRMIDSLNKNPADRFAMDEISQSL 622
Query 565 S 565
Sbjct 623 S 623

```

>ref|XP_002269408.1|  PREDICTED: hypothetical protein [Vitis vinifera]
Length=638

GENE ID: 100242712 LOC100242712 | hypothetical protein LOC100242712 [Vitis vinifera]

Score = 263 bits (673), Expect = 4e-68, Method: Compositional matrix adjust.
Identities = 176/574 (30%), Positives = 293/574 (51%), Gaps = 66/574 (11%)


```

Query 47 SCETYYVYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVDQVLLVPVTCGCT 106
      SC+ ++ + ++ P + +++IS++ + P +A+ +++ K +V+ VEV C C+
Sbjct 54 SCQAFLIFRSEPP-YNDVSSISDLLGSDPSQLAQINSVDETATFETKKEVI-VPVNCSCS 111
Query 107 GNRSFANISYEINQGDSEFYFVATTSYENLTNWRVMDLNPVLSFNKLPPIGIQVVFPLFCCK 166
      G S AN SY + GD++ +A ++E L+ +A+ L+ N + G ++ PL C
Sbjct 112 GEFSQANTSYVVQHGDTYLLIANNTFEGSLSTCQALRSQRTSLTTN-IYTGTKLTVPLRCA 170
Query 167 CPSKNQLDKEIKYLITYVVKPGDNVSLVSDKFGASPEDIMSENNYG-QNFTAANNLPVLI 225
      CP+RNQ D +KYL++Y+ GD VS +S +FG + N QN +LI
Sbjct 171 CPTKNQSDVGKYLMSYLVASGDYVSSISVRFGVDTGMTLEANELSEQNPNIYFPTLLI 230
Query 226 PVTRLP-----VLARSPSDGRKGGIRLPVIGISL-----GCTLLVLVLAVL 267

```


Sbjct	231	P+ LP ++ P SL G L++L +V+	290
Query	268	PLQNLPPSSSQITIVPPPPPPSPPTAVSSPSKSLKKTWVYVVVGVVAGSALVLLFGSVI	
Sbjct	291	LVVYVYCLMKMTLNRSASS-----AETADKLLSGVSGYVSKPTMYETDAIMEATMN	317
Query	318	+ K + A S E + L +S +Y+ + + AT N	
Sbjct	351	FFKFFRKRTRKKTDPAIASESFEACEKPLKEEQHEFLESISSIAQSLKVYKFEELQSATDN	350
Query	378	LSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNIKLMGVSSDNDGNCF	377
Sbjct	351	S C+I SVY+ I+G + A+K+ +V+ E+ +L K+NH N++L G+ NDG+ +	409
Query	378	FSPNCRIKGSVYRGTIKGDAAIKKMDGEVSNEIALLNKINHFNIRLSGICF-NDGHWY	437
Sbjct	410	VVYEYAENGSLDEWLFSSKSDTSNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHR	464
Query	438	+V+EYA NG L +W+++ + +SR L W QRI +A+DVA GL Y+H + P VH+	
Sbjct	465	LVHEYAVNGPLTDWIYN---NNDDSRF-LVWMQRIQIALDVATGLNLYHSYTSPPYVHK	471
Query	472	DITSSNILLDSNFKAKIANFSMARTFTNP-----MMP-----KI	
Sbjct	525	DI S N+LLDS+F+AKIANF +AR+ M P K+	524
Query	532	DIKSGNVLLDSDFRAKIANFGLARSAGQEQGFALTRHIITRGYMAPEYLENGLVSTKL	
Sbjct	583	DVFAFGVVLIELLTGRKAMTTKENGENVMLWKDIWKIFDQEEENREERLKKWMDPKLESYY	531
Query	583	DV+AFGV++E+LTG++ E GE + L D+ E + +E+L+ ++DP L Y	
Sbjct	583	DVYAFGVLMELEMTGKEVAALYE-GENMHL-PDVLVAVLHEGDGKEKLRNFIDPSLSGNY	582
Query	532	PIDYALSLASLAVNCTADKSLSRPTIAEIVLSLS 565	
Sbjct	583	P++ A+ + L +C SRP + EIV +LS 616	
Query	583	PLELAIVMIRLIDSCCLKKSPASRPDMVEIVQALS 616	

>ref|XP_002327712.1|  predicted protein [Populus trichocarpa]


gb|EEE75190.1|  predicted protein [Populus trichocarpa]
Length=630

GENE ID: 7464252 POPTRDRAFT_796841 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score = 258 bits (658), Expect = 2e-66, Method: Compositional matrix adjust.
Identities = 181/588 (30%), Positives = 297/588 (50%), Gaps = 90/588 (15%)

Query	47	SCETVYTYIAQSNFSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCT	106
Sbjct	42	SC+ Y+ + +Q P + ++ +IS + + P ++ +++ +Q+++VPV C C+	99
Query	107	SCQAYLIFRSQPP-YNTVASISTLLGSDPSQLSEVNSVSETT-SFPSNQLVIVPVNCSCS	
Sbjct	100	GNRSFANISYEINQGDSFYFVATTSYENLTNWRVMDLNPVLSFNKLPIGIQVVFPLFCK	166
Query	167	G S AN SY + D+ + +A +Y+ L+ +A+ + + + L G + PL C	
Sbjct	159	GEYSQANASYIVQPNDFLFIANNITYQGLSTCQALQNQKTRTRDDILS-GETLTVPLRCA	158
Query	226	CPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNY-GQNFTAANNLPVLI	225
Sbjct	219	CP+RNQ D I+YL++Y+ PGD+V +S++FGA+ + N QN T +LI	218
Query	257	CPTKNQSDLGIRYLLSYLVTPGDDVPAISEQFGAATGRTLEANGLEPQNPTIFFFTLLI	
Sbjct	275	FVTRLPLVLARS-----PSDGRKGGIRLPVIGISLG	256
Query	275	P+ P +++ G GGI L ++IG	
Sbjct	308	PLQSTPTSSQTVVPPPPPPASSPPSPSPNPEKSSKKTWLYVVVGVVGGIALTIVIG----	274
Query	308	CTLLVLVLA-----VLLVYVYCLMKMTLNRSASSAETADKLLSGVSGYVSKPTMYE	307
Sbjct	332	T++ +L+ V+ + K LN+ E + + +S +Y+	331
Query	332	-TIIFFMLSRKSKQPGFVIESQSFEAHEKPLNKKLD--EESQEFFESISAIAQSIKVYK	
Sbjct	368	TDAMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHGNIKLMG	367
Query	368	+ + AT N S C I SVY+ I G A+K+ DV++E+++L K+NH NL++L G	
Sbjct	392	FEDLKAATDNFSPSCWIKGSVYRGLINGDFAAIKKMNGDVSKEIELLNKINHNSNLIIRLSG	391
Query	428	VSSDNDGNCVFVYVYEAENGSLDEWLFSSKSDTSNSRASLTWCQRISMAVDVAMGLQYMH	427
Sbjct	446	V NDG+ ++VVEYA +G L +W++ D SN L W +RI +A DVA GL Y+H	445
Query	446	VCF-NDGHWYLVVEYAASGQLSDWIY-----DRSNEGKFLNWTKRIQIASDVATGLNLYH	
Sbjct	470	EHA-YPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNP-----MMP-	469
Query	505	YP VH+DI SSNILLDS+ +AKIANFS+AR+ + M P	
Sbjct	517	SFTNYPH-VHKDKSSNILLDSLRAKIANFSLARSTGDDQDEFVLTRHIVGTGKGYMAPE	504
Query	517	-----KIDVFAFGVVLIELLTGRK--AMTTKENGENVMLWKDIWK-IFDQEEENREE	
Sbjct	561	K+DV+AFG++ +E++TG++ A+ ++E+ + D+ + + +EE	517
Query	561	YLENGVSSKLDVYAFGILTLEIITGKEVAALHSEESRNL----SDVLNGALSEVDGQEE	560
Query	518	RLKKWMDPKLESYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSLS 565	
Sbjct	561	LK+ +DP L YP A+ + L +C RPT+ EIV SLs 608	

>ref|XP_002310777.1|  predicted protein [Populus trichocarpa]

gb|EEE91227.1|  predicted protein [Populus trichocarpa]
Length=643

GENE ID: 7477999 POPTRDRAFT_563086 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score = 254 bits (649), Expect = 2e-65, Method: Compositional matrix adjust.
Identities = 180/586 (30%), Positives = 289/586 (49%), Gaps = 84/586 (14%)

Query	47	SCETVYTYIAQSNFSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCT	106
Sbjct	53	SC+ Y+ + +Q P + ++ +IS + + P ++ +++ +Q+++VPV C C+	110
Query	107	SCQAYLIFRSQPP-YSTVASISTLLGSDPSQLSQINSVSETTS-FPTNQVLVLPVNCSCS	
Sbjct	111	GNRSFANISYEINQGDSFYFVATTSYENLTNWRVMDLNPVLSFNKLPIGIQVVFPLFCK	166
Query	167	G+ AN SY + G+ + +A +Y+ L+ +A+ + + N G + PL C	
Sbjct	170	GDYFQANASYIVQSGNTPFIIANNITYQGLSTCQAIRNEKGTRTVNIFA-GETLTVPLRCA	169
Query	226	CPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENNYGO-NFTAANNLPVLI	225
Sbjct	230	CP+RNQ D I+YL++Y+ GD VS+ +FGA + N + N T +LI	229
Query	226	CPTKNQSDLGIRYLLSYLVTWGDTVSIAGVRFADIGRALEANEISEKNPTIYFPTLLI	
Sbjct	230	FVTRLPLVLARS-----PSDGRKGGIRLPVIGISLGCTLLVLVLAV	266
Query	230	P+ P +++ SD + V +G ++G +L LV+	
Sbjct	230	PLKNPPTSSQTVVPPPPPPASPSPPSPSPNSDKSANKTWIYFVG-AVGIGIVLTIVIGT	288

```
Query 267 LLVYVYCLMKMT-----LNRSSASSAETADKLLSGVSGYVSKPTMYETD 309
++ ++ K K LNR E LL V +Y +
Sbjct 289 IIFFMLRKRKKQPGPIIVQSFEAHEKPLNRKLD--EEPQDLLESVYSIAQSIKVNYE 346


Query 310 AIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHNGLVKIMGVS 369
+ AT N S I SV++ I G A+K+ DV++E+ +L K+NH NL++L GV
Sbjct 347 DLKAATDNFSPFSFWIKSGSVFRGLINGDFAAIKKMNGDVSKEIDLKINHSNLIRLSGVC 406

Query 370 SDNDGNCFFVYEEYAENGSLDEWLFKSCSDTSSNRASLTWCQRISMAVDVAMGLQYMHEH 429
NDG+ ++VYEEA NG L +W++ +SN L W QRI +A DVA GL Y+H
Sbjct 407 F-NDGHWYLVYEEYAANGPLSDWIYV-----SSNEGKFLKWTQRIQIATDVATGLNYLHSF 460

Query 430 A-YPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNP-----MMP--- 469
YP VH+DI SSNILLD + +AKIANFS+AR+ P M P
Sbjct 461 TNYPH-VHKDIKSSNILLDKDLRAKIANFSLARSTDGPEGEFALTRHIVGTKGYMAPEYL 519

Query 470 -----KIDVFAFGVVLIELLTGRK--AMTTKENGEEVVMWKDIWK-IFDQEEENREERL 519
+KDV+AFG++ +E++TG++ A+ +EN E+ D+ + +E EE L
Sbjct 520 ENGIICFKLVDYAFGIILTLEIMTGKEVAALYREENREL----SDVLNGVLSEEGGLEESL 575

Query 520 KKWMDPKLESYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSL 565
+ +DP ++ YP A+ + L +C RP + EIV SL
Sbjct 576 SQLIDPSMQGNYPSPGLAVIMVRLIDSLCNKNPAGRPMAMDEIVQSLS 621
```

>ref|XP_002281880.1|  PREDICTED: hypothetical protein [Vitis vinifera]
Length=622

GENE ID: 100248852 LOC100248852 | hypothetical protein LOC100248852
[Vitis vinifera]

Score = 253 bits (647), Expect = 4e-65, Method: Compositional matrix adjust.
Identities = 178/567 (31%), Positives = 289/567 (50%), Gaps = 62/567 (10%)

```
Query 47 SCETYVYIIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCT 106
SC+ ++ + ++ P + S+ IS + ++P +AR +++++ + +V+ VPV C C
Sbjct 54 SCQAFILFKSEPP-YNSVPTISMLMSSNPGLARINSVKTLTVFPPTGKEVI-VPVNCSC 111

Query 107 GNRSFANISYEINQGDSEFYFV-ATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFC 165
G AN ++ I YF+ +Y+ L+ ++M N S L G+++ PL C
Sbjct 112 GQYYQANTTHIQDNQQTYFIIGNNTYQGLSTCDSLMRANR-YSEFSLSPGLELHVPLRC 170

Query 166 KCP SKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENYY--GQNFTAANNLP 223
C +++Q + KYL+TY DN + ++F S + I N +N T +
Sbjct 171 ACHTEHQAENGTKYLLTYSVSWEDNFPTIGERFNVSAKSIADANGLISEENPTIFPFTTI 230

Query 224 LIPVTRLPLVLA-----SPSDGRKGIRLPVIIGISLGTLL--VLVL 264
LIP+ P+ ++ S S + R+ + GI+ GC LL V+
Sbjct 231 LIPKTEPLSSQTKTHATQPVLDPPPTSDSGSSRSKRRIYLGAGIAAGCFLLGPSVIFS 290

Query 265 AVLLVYVYCLMKMTLNRSSASSAETADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKI 324
V L Y K + + + LL ++ P ++E + +AT N S + +I
Sbjct 291 IVFLFYKKRSKKVPPVHGKTKSVLPEDLLVEIASVDPVPKVFEFKKLKKATGNFSSKSRI 350



Query 325 GESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHNGLVKLMGVSSDNDGNCFFVYEEYA 383
V++A + +++AVK+ K D++EE+ IL K+NH NL+KL GV +G+CF +V+EY
Sbjct 351 KGCVFRAELGREIVAVKKMKVDISEEVNILNHNHNLIKLHGVC--KNGSCFYLVFEYM 408

Query 384 ENGLDEWLFKSCSDTSSNRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSN 443
ENGL EWL +S S S +W +RI +A+DVA GL Y+H P VH+ I SSN
Sbjct 409 ENGLRLEWHKES-----SNHSQSWSKRIQIALDVANGLHYTHNFTKPAYVHKHKSSN 462

Query 444 ILLDSNFKAKIANFSMART-----FTNP-----MMPKIDVFAFG 477
ILL N +AKIANFS+ART + P + PK+DV+AFG
Sbjct 463 ILLTKNIRAKIANFSLARTAVKGAKTHALNMLVVGTRGYMAPEYIEAGSITPKVDVYAFG 522

Query 478 VVLIELLTGRKAMTTKENGEEVVMWKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYAL 537
VV++EL+TG+ A+ +N E V+L + + I ++ N E L ++DP L I+ A
Sbjct 523 VVMLELITGKDAVII-QNEEEVLLSEAMISIMER-GNAEIELGHFLDPCLLGNNGIESAT 580

Query 538 SLASLAVNCTADKSLSRPTIAEIVLSL 564
+A L++ C RP++ E+V +L
Sbjct 581 RIAKLSIACLTQDQARRPSMGEVVSTL 607
```

>ref|XP_002509540.1|  ATP binding protein, putative [Ricinus communis]
gb|EEF50927.1|  ATP binding protein, putative [Ricinus communis]
Length=681

GENE ID: 8271475 RCOM_1677900 | ATP binding protein, putative
[Ricinus communis]

Score = 253 bits (647), Expect = 4e-65, Method: Compositional matrix adjust.
Identities = 201/621 (32%), Positives = 299/621 (48%), Gaps = 104/621 (16%)

```
Query 44 SPSCETYVYIIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTC 103
S C+T+ ++ + F SL+N+S + IA A+ + L KDQ LL+P+ C
Sbjct 49 SQDHCKTFAI-LSTNSYFSSLSNLSFYLGFNRFVIAEANGFSADTEFLPKDQPLLIPIDC 107

Query 104 GCTGNRSFANISYEINQGDSEFYFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVFPL 163
C GN A ++ +G++FY +A S E LT +A+ + N +SP L +++ PL
Sbjct 108 KCGNFFRAEVRFTTKTIKGENFYGIAE-SLEGLTTCIAIQENNLGVSPWNLADKARLLVPL 166

Query 164 FCKCPSKNQLDKEIKYLITYVWKPGDNVSLVSDKFGASPEDIMSENYYG-QNFTAANNLP 222
C CPS +Q+ ++L++Y GD +S ++ KF +PE I+S NN NF N +P
Sbjct 167 RCACPSSQGTALATRFLLSYFVSEGDITISNIAIKFNTTPEAIISANNRSLANFKPENLVP 226

Query 223 ---VLIPVTRLPLVA-----RSP-SDGRKGIRLPVI-----IGISLGTLLV- 261
+LIP+ R P L R P S R+ I PVI IG+ + T +V
Sbjct 227 LASLLIPLNREPALGSLAKPREPNPFPRESSI--PVINPHKKKSKMMIGVYIAVTGVVV 284






Query 262 -----LVLA VLLVYVYCLMKMTLNR-----SASSAETADKLLS--GVSGYVSKPTM 305
+V A L+V + K + L++ S S T+K+S G + +
Sbjct 285 GATIAIVAFLIVQLKKKKKQNL SKDGPQLQSLSVRTTSEKKVSFEQSQQDLDNQII 344

Query 306 -----YETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELK 352
```

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      Y  + + +AT + S      I  SVY  + GK LA+KR K +  ++
Sbjct  345  DTTPRNRKVLVENTVEELRKATEDFSSSSSLIDGSVYVYGRINGKNLAIKRTKSETISKID  404
Query  353  ILQKVN-----HGNLVKLMGVSSDNDGNCFFVVEYAENGSLDEWL-----FSKSCSD  399
      N  H N++L+G      + F+V+EYA+NGSL +WL      F  SC
Sbjct  405  FSHFQNATHHHHPNIIIRLLGTCLSEGSDFLVFEYAKNGSLKDWLHGGLAMKNQFIASC--  462
Query  400  TSNRSASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSM  459
      LTW QR+ + +DVA+ LQYMH      P  VHR++ S NI LD  F AKI NF M
Sbjct  463  ----YCFLTWNQRLKICLDVAVALQYMHIMNPSYVHRNVKSRNIFLDEEFNAKIGNFGM  518
Query  460  ARTF-----TNP-----MMPKIDVFAFGVVLLIELLTGRKAMT  491
      AR      TNP      + P  ID+FAFGVVL+E+L+G++ +T
Sbjct  519  ARCIEGDTQNTIEHSTNPFSSWSLGYLAPEYIHQGVSPCIDIFAFGVVLLEVLSGKRPIIT  578
Query  492  TKEN-GEVVMLWKDIWKIFDQEEENREERLKKWMDPKLESYYPIDYALSLASLAVNCTADK  550
      +N GE  L + K      EN  E L++WMD  L  Y  D A++LA+LA +C ++
Sbjct  579  RPDNKGEESSLSEKMKSLSSSENAGE-LREWMDNALGENYSFDTAVTLANLARSCVEEE  637
Query  551  SLSRPTIAEIVLSLSLLTQPS  571
      RP  E+V  LS L + S
Sbjct  638  PSLRPNAGELVEKLSRLVEES  658

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>ref|NP_001058110.1|  Os06g0625200 [Oryza sativa Japonica Group]
 dbj|BAD35689.1|  receptor protein kinase-like [Oryza sativa Japonica Group]
 dbj|BAD37734.1|  receptor protein kinase-like [Oryza sativa Japonica Group]
 dbj|BAF20024.1|  Os06g0625200 [Oryza sativa Japonica Group]
 gb|EAZ37689.1|  hypothetical protein OsJ_22029 [Oryza sativa Japonica Group]
 Length=630



GENE ID: 4341567 Os06g0625200 | Os06g0625200 [Oryza sativa Japonica Group]
 (10 or fewer PubMed links)

Score = 251 bits (640), Expect = 3e-64, Method: Compositional matrix adjust.
 Identities = 170/578 (29%), Positives = 297/578 (51%), Gaps = 86/578 (14%)

```

Query  47  SCETYVITYIAQSPNFLSLTNISNIFDTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCT  106
      SC  Y+T+ + P      +++ + + +P ++A A+++      + Q+LLVPV C C
Sbjct  56  SCTAYLTFRSDPP-----LSVAYLLNATPSAFAAANSVPLAVSPVDGTQLLLVPVPCSC-  109
Query  107  GNRSFA----NISYEINQGDSFYFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVPF  162
      NR+      N +Y I + D+F+ +A  +++ LT +++++ NP      I  + P
Sbjct  110  -NRATGYQHNNTYAIGELDTFFLIANNTFQGLTTYQSIIANPASEAMSPVINGPLAVP  168
Query  163  LFCKCPSKNQLDKEIKYLITYVVKPGDNVSLVSDKFGASPEDIMSENNYGQNFTAANNLP  222
      L C CPS      I  L+TYV + GDNV+ ++ +F ++  D+++ N
Sbjct  169  LRCACPSATT--GRINNLLTYVVQEGDNVTSIARRFNSTHGDVLAANT-----  214
Query  223  VLIPVTRLP-----VLARSPSDGRK-----GGIRLPVIIGISLGCTLLVLVL  264
      +L+P+      P  + + +P + +K      G+  + IG+  G +  VL
Sbjct  215  LLVPLVHPHPSRVVLANTTITSTTPPESQKFYVSSPCSNGLLAGLGIGVGCWSAWAAVL  274
Query  265  AVLLVYVYCLKMTLNRSASSAETADKLLSGVSGYVSKPTMYETDAIMEATMNLSEQCKI  324
      AV L++      + S + ET  L++ V G V      Y  I  AT  +E+ ++
Sbjct  275  AVFLLWRRRRRRRVPVGDSSGMARET--PLVAAVRGAVETLAAYSADIETATAGFAEERRV  332
Query  325  --GESSVKANIEGKVLAVKRK---EDVTEELKILQKVNHGSLVGLMGVSSDNDGNCFFV  379
      G SVY+A I G+  AVKR      +DV  E+ +L +VNH  LV+L G+ ++ D + ++V
Sbjct  333  AAGSSVYRAVINGEAFVAVKVAAGGDDVRGEVDVLRVNHSGLVRLRGLCANGD-DTYLV  391
Query  380  YEYAENGSLDEWLFSKSCSDTNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRDI  439
      E+AENG+L EWL  S + + R  L W QR+ +A+DVA GL Y+H      P  VH+++
Sbjct  392  LEFAENGALSEWLHFGSAA--ACLRRLVGWKQRVLVALDVAGGLNYLHHFTNPYPVHKNL  449
Query  440  TSSNILLDSNFKAKIANFSM-----ARTFTNP-----MM  468
      S N+LLD+N +AK+++      + P      +
Sbjct  450  NSGNVLLDANLRAKVVSLGFARAVAVAVAAGDSDSIALMTHHVVGTHGYLAPEYLEHGLIS  509
Query  469  PKIDVFAFGVVLIELLTGR-KAMTTKENGEEVVMLWKDIWKIFDQEEENREERLKKWMDPKL  527
      PK+DVFF+FGV+ +ELL+G+ A T ++G+ ++LW+      + D +      +L+ +MDP+L
Sbjct  510  PKLDVFSFGVIQLELLSGKTAFAVTDGQNMMLWQAADGLVDG-DGAWFKLRAFMDPQL  568
Query  528  ESYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSLS  565
      + +YPI A ++A+LAV C A +  +RP++ E+ ++LS
Sbjct  569  QGHYPIGVASAVAALAVRCVAREPRARPSMEEVFVTL  606

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>ref|XP_002307830.1|  predicted protein [Populus trichocarpa]
 gb|EEE94826.1|  predicted protein [Populus trichocarpa]
 Length=659

GENE ID: 7479122 POPTRDRAFT_862283 | hypothetical protein [Populus trichocarpa]
 (10 or fewer PubMed links)

Score = 248 bits (632), Expect = 2e-63, Method: Compositional matrix adjust.
 Identities = 170/589 (28%), Positives = 295/589 (50%), Gaps = 82/589 (13%)

```

Query  47  SCETYVITYIAQSPNFLSLTNISNIFDT--SPLSIARASNLEPMDDKLVKDQVLLVPVTCG  104
      SC++Y+T+ + P + S  I+ +      S  IA +NL      + + ++VPV C
Sbjct  58  SCQSYLTFRSMPP-YNSPVLIAYLGLVFPQSATRIASINNLSSTATIPTNTQVVVPVNC  116
Query  105  CTGNRSFA-NISYEI-NQGDSFYFVATTSYENLTNWRVMDLNPVLSPNKLPIGIQVVPF  162
      C + + N +Y++ ++ +++++ VA  +Y+ LT  +++M NP      N L +G+ + P
Sbjct  117  CYARQYQHNSTYQLKDKSETYFSVANNTYQGLTTCQSLMSQNPYGRDN-LSLGLTLQIP  175
Query  163  LFCKCPSKNQLDKEIKYLITYVVKPGDNVSLVSDKFGASPEDIMSENNYGQNFTAANNLP  222
      L C CP+ NQ      I  +L+TY+  GD++S ++  FG  ++ N      + P
Sbjct  176  LRCACPNSNQNASINHLTYMVTWGDSSISIAQLFGVDQQRVLDANKLSSSIIFPFTP  235
Query  223  VLIPVTRLPLV-----LARSPSDGRKGGI-RLPVIIGISLGCTLLVLVLAVL  267
      +L+P+      P  ++P+      G  + +G+ +G  L+L+ A
Sbjct  236  ILVPLPTEPTKIEQPSAAPPAPSPQTPNVSVGGSSDHKALYVGVGIGAAFLILLFAAF  295

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Query   268  LVVYVCLMKMTLNRSSASSAETADKLLSGVSGYVSKP-----TMY 306
          + K + + S++E + L S + + P T+Y
Sbjct   296  GFLFWHRKSRKQKQPVSTSE-PETLPSVSTDFTVLPVSNKNSWSLSSHADARYAIESLTVY 354

Query   307  ETDAIMEATMNLSEQCKIGESVYKANIEGKVLAVKRFKEDVTEELKILQKVNHNGLVKLM 366
          + + + AT ++ I SVY+ + +G AVK K DV+ E+ IL+ +NH N+++L
Sbjct   355  KYEDLQVATGYFAQANLIKSGSVYRGSEFKGDTAAVKVVKGDVSSSEINILKMINHSNVIRLS 414

Query   367  GVSSDNDGNCFFVVEYEAENGSLDEWLFSSKSCSDTSNSRASLTWCQRISMAVDVAMGLQYM 426
          G ++GN ++VVEYA+NGSL +WL S +N L W QR+ +A DVA L Y+
Sbjct   415  GFCL-HEGNTYLVVEYADNGSLTDWLHS-----NNIYRILAWKQRVRIAYDVADALNYL 467

Query   427  HEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNP----- 466
          H + P +H+++ +SNILLD+N +AK+ANF +ART N
Sbjct   468  HNYTNPSYIHKNLKTSNILLDANLRKAVANFGLARTLENGQDGGQLQTRHVVGTVQGYLAP 527

Query   467  -----MMPKIDVFAFGVVLIELLTGRKAMTT---KENGEVVMWVKDIWKIFDQEEENRE 516
          + PK+DVFAFGVV++ELL+G++A T K G+ +L I ++ + +N
Sbjct   528  EYIENGWITPKLDVFAFGVVMLELLSGKEAAATAIDKIAGD-DLLSVMIMRVL-EGDNVR 585

Query   517  ERLKKWMDPKLESYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSLS 565
          E+L ++DP L YP+D A S+A LA +C +RP++ ++ + LS
Sbjct   586  EKLSAFLDPCLRDEYPLDLAFSMAQLAKSCVEHDLNTRPSPMPQVFMMLS 634

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>emb|CA002961.1| LysM-domain containing receptor-like kinase [Medicago truncatula var. truncatula]
Length=131

Score = 240 bits (613), Expect = 4e-61, Method: Composition-based stats.
Identities = 111/130 (85%), Positives = 121/130 (93%), Gaps = 0/130 (0%)

```


Query   412  RISMAVDVAMGLQYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSMARTFTNPMPMKI 471
          RI++A+DVA+GLQYMHEH YPRI+HRDIT+SNILL SNFKAKIANF MART TN MMPKI
Sbjct   1      RITIAMDVATIGLQYMHEHTYPRIIHRDITTSNILLGSNFKAKIANFGMARTSTNSMMPKI 60

Query   472  DVFAFGVVLIELLTGRKAMTTKENGEVVMWVKDIWKIFDQEEENREERLKKWMDPKLESYY 531
          DVFAFGVVLIELLTG+KAMTTKENGEVV+LWKD WKIFD E NREERL+KWMDPKLES+Y
Sbjct   61      DVFAFGVVLIELLTGKKAMTTKENGEVVILWKDFWKIFDLEGNREERLRKWMDPKLESFY 120

Query   532  PIDYALSLAS 541
          PID ALSLAS
Sbjct   121  PIDNALSLAS 130

```

>ref|XP_002300098.1|  predicted protein [Populus trichocarpa]

gb|EEE84903.1|  predicted protein [Populus trichocarpa]
Length=680

GENE ID: 7467712 POPTRDRAFT_641782 | hypothetical protein [Populus trichocarpa]
(10 or fewer PubMed links)

Score = 238 bits (607), Expect = 2e-60, Method: Compositional matrix adjust.
Identities = 196/650 (30%), Positives = 304/650 (46%), Gaps = 104/650 (16%)

```

Query   14  ILCLVIMLFSTNIVA-QSQQDNRTNFSCPSDS-PPSCETYVTYIAQSPNFLSLTNISNIF 71
          ++CL++ N+++ Q+ + + + C S+ C+T+ + S F SL+N+S
Sbjct   19  LICLLVSALGQNLSCQTTSFDPASGYHCNSNGLQDQCKTFAI-LHTSSYFSSLSNLSFYL 77

Query   72  DTSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSEFYFVATTS 131
          IA + + L KDO LL+P+ C C G A ++ +G+SFY + + S
Sbjct   78  GLDRFVIAATNGFSANTEFLPKDQPLLPIDCKCNGGFFQALVTKTTIKGESFYISI-SKS 136

Query   132  YENLTNRWRAVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYVWKPQDNV 191
          E LT +A+ + NP +SP L +Q+ PL C CPS ++ + L++Y GD +
Sbjct   137  LEGLTTCATREKNPGISPENLNGKVQLQVPLRCACPSSTEIVILATRLLLSYPVSAAGDTI 196

Query   192  SLVSDKFGASPEDIMSENN-----YGQNFT----AANLNPVL-IP 226
          S ++ KF +PE I S NN G T A N P L IP
Sbjct   197  SNLAIKFNTTPEAITSANNRSLTTFKPTSLVPLTSLLIPLGGKPTLGLAKPNEPNLHIP 256

Query   227  VTRLPVLARSFSDGRKGGIRLPVIGISLGCTLLVLVLAVLLVYVYCLMKMTLNRSSASSA 286
          + LPV+ +P R R+ V I ++ + +A + + K K + +
Sbjct   257  ASSLPVI--NPHKKRSKMWRIGVYIAVTGAVVGVSIAIAAAFLVIQLKKKQVLSKEADT 314

Query   287  E-----TADKLLS---GVSGYVSKPT-----MYETDAIMEATMNLSEQCK 323
          E T+DK +S + + S+ T Y + + AT + + +
Sbjct   315  ELQQLSLSVRTTSDKKVSFDDSQNHFDQSITDTTPGKVFVETYTVEELKRATEDFNSSNQ 374

Query   324  IGESVYKANIEGKVLAVKRFKEDVTE--ELKILQKV--NHGNLVKLMGVSSDNDGNCFFV 379
          I SVY + GK LA+KR + + EL + Q +H N+++++G + F+V
Sbjct   375  IEGSVYHGRLNGKNLAIKRVQPETISKVELGLFQDATHHHFNIIRVVGTCCLSEGPDSFLV 434

Query   380  YEYAENGSLDEWL-----FSKSCSDTSNSRASLTWCQRISMAVDVAMGLQYMHEHA 430
          +EYA+NGSL +WL F SC LTW QR+ + +DVA+ LQYMH
Sbjct   435  FEYAKNGSLKDLHGGGLAMKNQFIASC-----YCFLTWNQRLKICLDVAVALQYMHIM 488

Query   431  YPRIVHRDITSSNILLDSNFKAKIANFSMARTF-----TNP-----MMPK-- 470
          +P VHR+I S NI LD F AKI NF MA TNP + P+
Sbjct   489  HPSVYHRNIKSRNIFLDEEFNAKIGNFGMAGCVEDDTKEPDPFNSTNPASWSLGLYLAPEAH 548

Query   471  -----IDVFAFGVVLIELLTGRKAMTT-KENGE-VVMWVKDIWKIFDQEEENREERLKK 521
          D+F+FGVVL+E+L+G+ +T +NGE + L K I I EN +E L++
Sbjct   549  QGVVSSSTDIFSGVVLMEVLSGQTPITRPNDNGEGSIWLSKKIKSIL-LENADE-LRE 606

Query   522  WMDPKLESYYPIDYALSLASLAVNCTADKSLSRPTIAEIVLSLSLLTQPS 571
          W+D + Y D A +LA++A CT + RPT EIV L L + S
Sbjct   607  WIDSAMGENYSFDEAATLANIARACTEEDPSLRPTSGEIVEKLLRLVEES 656

```

>ref|NP_566689.2|  CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/ receptor signaling protein/ transmembrane receptor protein kinase [Arabidopsis thaliana]

dbj|BAF92788.1|  chitin elicitor receptor kinase 1 [Arabidopsis thaliana]

Length=617

GENE ID: 821717 CERK1 | CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/
receptor signaling protein/ transmembrane receptor protein kinase
[Arabidopsis thaliana] (10 or fewer PubMed links)


Score = 236 bits (602), Expect = 8e-60, Method: Compositional matrix adjust.
Identities = 163/535 (30%), Positives = 270/535 (50%), Gaps = 74/535 (13%)

Query	89	DKLVKDQVLLVPVTCGCT-GNRSFANISYEINQGDSEFYFVATTSYENLTNWRVMDLNPV	147
		D++ +LVP C C G+ N SY + Q D++ VA ++Y NLT ++ NP	
Sbjct	77	DRIQMGSRVLVFPFCECQPGDFLGHNFYSYVRQEDTYERVAISNYANLTTMESLQARNPF	136
Query	148	LSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYVWKPGDNVSLVSKFGASPEDIMS	207
		+ N +P+ + + C C ++ + K+ +TY +P D++S ++ G S DI+	
Sbjct	137	PATN-IPLSATLNLVNLVNCSCGDES-VSKDFGLFVTYPLRPEDSLSSIARSSGVSA-DILQ	193
Query	208	ENNYGQNFTAANNL---PVLI PVTRLFVLARSPSDGRKGGIRLFPVIIGISLGCTLLVLVL	264
		N G NF + N + P P P S DG G VI GI +G + +L++	
Sbjct	194	RYNPGVNFNSGNGIVYVPGRDPNGAFPEFKSSKQDGVGAG---VIAGIGIVVALLLI	249
Query	265	AVLLVYVYC-----LKMKTNLRSASSAETADKLLSGVSGYVS-----KPTM	305
		++ Y Y L K + S++S ++ +GVS ++ K	
Sbjct	250	LFIVYYAYRNKNSKGDSESSSIPLSTKADHASSTSLQSGGLGGAGVSPGIAAISVDKSVE	309
Query	306	YETDAIMEATMNLSEQCKIGE----SVYKANIEGKVLAVKRFKEDVTE----ELKILQKV	357
		+ + + +AT N + KIG+ +VY A + G+ A+K+ + ++ ELK+L +V	
Sbjct	310	FSLEELAKATDNFNLSFKIGQGFGAVYYAELRGEKAAIKMDMEASKQFLAELKVLTRV	369
Query	358	NHGNLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSKSCSDTSNSRASLTWCQRISMAV	417
		+H NLV+L+G + G+ F+VVEY ENG+L + L + R L W +R+ +A+	
Sbjct	370	HHVNLVRLIGYCV--GSLFLVYEYVENGNLGQHLHG-----SGREPLFPWTKRVQIAL	420
Query	418	DVAMGLOYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFMSMAR-----	461
		D A GL+Y+HEH P VHRDI S+NIL+D F+AK+A+F + +	
Sbjct	421	DSARGLEYIHEHTVPVYVHRDIKSANILIDQKFRKAVADFGLTKLTEVGGSATRGAMGTF	480
Query	462	-----TFTNPMMPKIDVFAFGVVLIELLTGRKAMTTKENGEVVMLWKDIWKIFDQ---E	512
		T + K+DV+AFGVVL EL++ + A+ E V ++ + +F++ E	
Sbjct	481	GYMAPETVYGEVSAKVDVYAFGVVLYELISAKGAVVKMT--EAVGEFRGLVGVEESFKE	538
Query	513	ENREERLKKWMDPKLESYYPIDYALSASLAVNCTADKSLSRPTIAEIVLSLSLL	567
		+EE L+K +DP+L YP D +A L CT + + RP++ IV++LS L	
Sbjct	539	TDKEEAARKIIDPRLGDSYPFDSVYKMAELGKACTQENAQLRPSMRVIVVALSTL	593

>emb|CB140054.3| unnamed protein product [Vitis vinifera]
Length=672

Score = 234 bits (598), Expect = 2e-59, Method: Compositional matrix adjust.
Identities = 181/631 (28%), Positives = 297/631 (47%), Gaps = 69/631 (10%)

Query	14	ILCLVIMLFSTNIVAQQQDNRTNFSCPSD-SPPSCETYVTYIAQSPNFLSLTNISNIFD	72
		IL V L + + ++ + + + C + S C T+ S + SL N+S	
Sbjct	17	ILVVFVSLGQSLLSCESTSSRDASGYCNGNGSQKQCGTFALLRTNS-YYSSLFNLSFYLG	75
Query	73	TSPLSIARASNLEPMDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGDSEFYFVATTSY	132
		IA A+ + L + LL+P+ C C A ++ +G+SF+ +A S	
Sbjct	76	IDRFLIAEANGFSADTELLPYNLPLLIPIECKCKAGFFQAEELTKTTTEGESFFGIAE-SL	134
Query	133	ENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCKCPSKNQLDKEIKYLITYVWKPGDNVS	192
		E LT +A+ + NP + P L +++ PL C CPS ++L +E K L++Y GD V	
Sbjct	135	EGLTTCKAIRERNPSIQPWGLADKVRLLIPLRCACPSSSELIQETKLLLSYPVSEGDTVP	194
Query	193	LVSKFGASPEDIMSENNY-GQNFTAANNLP--VLIPVTRLFVLARSPSDGRKGGIRLPV	249
		++ KF + E I+S NN G + P + +P T+PV+ +P + ++ V	
Sbjct	195	SLAFKFNTTSEAIISANNRSGATLRLGSLAPPNLGLPATSIPIV--NPHKKKTKMWKIGV	252
Query	250	II---GISLGCTLLVLVLAVLLVY-----VYCLKMKMTNLRSASSAETA	289
		I G+++G ++ + AVL+++ L ++T + S E +	
Sbjct	253	YIAVSGVAVGASV-AIAAAVLVIHWRKKQNAYKMGDVELQQGLSVRTTSEKKVSFEFS	311
Query	290	DKLLSGVSGYVSKPTMYETDAIME---ATMNLSEQCKIGESVYKANIEGKVLAVKRFKED	346
		+ + + ET ++E AT + + I SV+ + GK LA+K +	
Sbjct	312	QDPIDQIIDSTPHKIVVETYTMLELRKATEDFNSSNIEGVSFVHGRNLGNKLAIKHTHE	371
Query	347	VTE--ELKILQKV--NHGNLVKLMGVSSDNDGNCFFVVEYAENGSLDEWLFSKSCSDT--	400
		E + +H N+++L+G + + +++EYA+NGSL +WL +	
Sbjct	372	AISKIEFLFHDAIHHPNIMRLLGTCLNEGPDYSLIFEYAKNGSLKDWLHGGLAMKSQF	431
Query	401	-SNSRASLTWCQRISMAVDVAMGLOYMHEHAYPRIVHRDITSSNILLDSNFKAKIANFSM	459
		++ LTW QR+ + +DVAM LQYMH +P VHR+I S NI LD F AKI NF M	
Sbjct	432	IASCYCFLTWNQRLRICLDVAMALQYMHMHPCYVHRNIKSRIPLDEEFNAKIGNFGM	491
Query	460	ARTFTNP-----MMPKIDVFAFGVVLIELLTGRKAMTTK	493
		AR F + + P +D+FA+GVVL+E+L+G+ +T	
Sbjct	492	ARCFEDDAEDSQPYSTASWSKGYLAPEYLHQGIISPTLDIFAYGVVLEVLSGKTPITRA	551
Query	494	EN--GEVVMLWKDIWKIFDQENREERLKKWMDPKLESYYPIDYALSASLAVNCTADKS	551
		++ G V L + I I E E L+ WMD L Y D A++LA+LA CT +	
Sbjct	552	DDKGGGRVWLPEKIKSILGSENT--EELRDWMDSALGENYSFDAAITLANLARVCTDENP	609
Query	552	LSRPTIAEIVLSLSLLTQPSPATLERSLTSS	582
		SRP+ EIV LS L + P + S+ S	
Sbjct	610	CSRPSAGEIIVEKLSRLVEQLPEGEQFSICES	640

>ref|XP_002263070.1|  PREDICTED: hypothetical protein [Vitis vinifera]
Length=675

GENE ID: 100264694 LOC100264694 | hypothetical protein LOC100264694
[Vitis vinifera] (10 or fewer PubMed links)

Score = 233 bits (595), Expect = 4e-59, Method: Compositional matrix adjust.
Identities = 185/652 (28%), Positives = 298/652 (45%), Gaps = 89/652 (13%)

Query	14	ILCLVIMLFSTNIVAQQQDNRTNFSCPSD-SPPSCETYVTYIAQSPNFLSLTNISNIFD	72
-------	----	---	----

Sbjct	17	IL V L + + ++ + + + C + S C T+ S + SL N+S	75
Query	73	ILVVFVSTLGQSLLSCE TSSRDASGYCNGNGSQKQCGT FALLRTNS-YYSSLFNLSFYLG	
Sbjct	76	TSPLSIARASNLEPMDDKLVKDQVLLVPVTCGCTGNRSFANISYEINQGD SFYFVATTSY	132
Query	133	IA A+ + L + LL+P+ C C A ++ +G+SE+ +A S	
Sbjct	135	IDRFLIAEANGFSADTELLPYNLPLLIPIECKCKAGFFQAE LTKTTIEGESFFGIAE-SL	192
Query	193	ENLTNWRVMDLNPVLSPNKLPIGIQVVFPLFCCKCP SKNQLDKEIKYLITYVWKPGDNVS	194
Sbjct	195	E LT +A+ + NP + P L +++ PL C CPS ++L +E K L+Y GD V	
Query	249	EGLTTCKAIRERNPSIQFWGLADKVRLLIPLRCACPSSELIQETKLLLSYPVSEGDTVP	248
Sbjct	253	LVSDKFGASPEDIMSENNY-CQNFTAANNLPV---LIPVTRLPV LARSPSDGRKGGIRLP	
Query	271	++ KF + E I+S NN G + FV LIP+ P L SP+ R+ + LP	253
Sbjct	276	SLAFKFNTTSEAITISANNRSGATLRLGSLAPVSSLLIPLRDKPTLG-SPAKPREPNLGLP	
Query	313	V-----IIGISLGCTLLVLVLAVLLVY-----	270
Sbjct	317	+ G+++G ++ + AVL+++	
Query	325	ATSPVPINPHKKKTKMWKIGVYIAVSGVAVGASV-AIAAAVLVIHWKRKKQNAYKMGDVE	312
Sbjct	326	--VYCLMKMTLNRSASSAETADKLLSGVSGYVSKPTMYETDAIME---ATMNLSEQCKIG	
Query	332	L ++T + S E + + + + ET ++E AT + + I	325
Sbjct	333	LQQLGLSVRTSEKKVSEFGSQDPIDQIIDSTPHKIVVETYTMLELRKATEDFNSSNLIE	372
Query	373	ESVYKANIEGKVLAVKRFEKEDVTE--ELKILQKV--NHGNLVKLMGVSSDNDGNC FVVYE	381
Sbjct	376	SV+ + GK LA+K + E + +H N+++L+G + + ++++E	
Query	382	GSVFHGRNLNGK NLAIKHTHPEAISKIEFGLFHDAIHHPNIMRLLGTCLNEGPD SYLIFE	432
Sbjct	383	YAENGSLDEWLF SKSCSDT---SNSRASLTWCQRISMAVDVAMGLQYMHEHAYPRIVHRD	
Query	432	YA+NGSL +WL + ++ LTW QR+ + +DVAM LQYMH +P VHR+	438
Sbjct	433	YAKNGSLKDWLHGGLAMK SQFIASCYCFLTWNQRLRICLDVAMALQYMHMHMPCYVHRN	492
Query	473	ITSSNILLDSNFKAKIANFSMARTETNP-----MMPKID	472
Sbjct	476	I S NI LD F AKI NF MAR F + + P +D	
Query	531	IKSRNIFLDEEFNAKIGNFGMARCFEDDAEDSQPYSTASWSKGYLAPEYLHQGIISPTLD	552
Sbjct	533	VFAFGVVLIELLTGRKAMTTKEN--GEVVMLWKDIWKIFDQEE NREERLKKWMDPKLESY	
Query	553	+FA+GVVL+E+L+G+ +T ++ G V L + I I E E L+ WMD L	530
Sbjct	556	IFAYGVVLEVLVSGKTPITRADDKGGGRVWLPEKIKSILGSENT--EELRDWMDSALGEN	610
Query	582	YPIDYALSASLAVNCTADKSLSRPTIAEIVLSLSLLTQPSPATLERSLTSS	
Sbjct	583	Y D A++LA+LA CT + SRP+ EIV LS L + P + S+ S	582
Query	611	YSFDAAITLANLARVCTDENPCSRPSAGEIVEKLSRLVEQLPEGEQFSICES	662

Select All [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#)

APPENDIX C

Claim	Type	Depends from	%ID	AA SEQ ID	NA SEQ ID
59.	AA	-	80 AA	8 15 31 32 40 48	-
60.	AA	-	80 AA	24 25	-
61.	AA	59	100 AA	8 15 31 32 40 48	-
62.	AA	60	100 AA	24 25	-
63.	AA-combo	59 + seq	80/80 AA	8 15 31 32 40 48/ 24 25 52 54	-
64.	AA-combo	61(59)	100/100 AA	8 15 31 32 40 48/ 24 25 52 54	-
65.	NA	59	80 AA	ENC 80%[8 15 31 32 40 48]	-
66.	NA	60	80 AA	ENC80%[24 25]	-
67.	NA	65 (59)	100 NA	[encode 80% 8 15 31 32 40 48]	6 7 11 12 30 39 47
68.	NA	66 (60)	100 NA	[encode 80% 24 25]	21 22 23
69.	Tg cell NA	59	80 AA	[encode 80% 8 15 31 32 40 48]	-
70.	Tg cell NA	69(59)	100 AA	[encode 100% 8 15 31 32 40 48]	-
71.	Tg cell NA	69(59)	100 NA	[encode 80% 8 15 31 32 40 48]	6 7 11 12 30 39 47
72.	Tg cell NA	60	80 AA	ENC80%[24 25]	-
73.	Tg cell NA	72(60)	100 AA	ENC100%[24 25]	-
74.	Tg cell NA	72(60)	100 NA	ENC 80%[24 25]	21 22 23
75.	Tg cell NA	63(59)	80/80 AA	[enc 8 15 31 32 40 48/ 24 25 52 54]	-
76.	Tg cell NA	63(59)	100/100 AA	[enc 8 15 31 32 40 48/ 24 25 52 54]	-
77.	plant cell	Xxx			
78.	plant cell	Xxx			
79.	plant cell	Xxx			
80.	plant cell	Xxx			
81.	plant cell	Xxx			
82.	plant cell	Xxx			
83.	plant cell	Xxx			
84.	plant cell	Xxx			
85.	method	59	80 AA	8 15 31 32 40 48	-
86.	method	85(59)	100 AA	8 15 31 32 40 48	-
87.	method	85(50)	100 NA	[encode 80% 8 15 31 32 40 48]	6 7 11 12 30 39 47
88.	method	60	80 AA	24 25	-
89.	method	88 (60)	100 AA	24 25	-
90.	method	88(60)	100 NA	[encodes 80% 24 25]	21 22 23
91.	method	85(59)	80/80 AA	[8 15 31 32 40 48/ 24 25 52 54]	-
92.	method	86 (85)(59)	100/100 AA	[8 15 31 32 40 48/ 24 25 52 54]	-
93.	method	91(85)(59)	100 NA	[encodes 80% 8 15 31 32 40 48/ 24 25 52 54]	6 7 11 12 30 39 47/ 21 22 23 51 53
94.	Method x	85(59)	80 AA	8 15 31 32 40 48	-
95.	Method x	88(60)	80 AA	24 25	-
96.	Method x	91(85)(59)	80/80 AA	[8 15 31 32 40 48/ 24 25 52 54]	-
97.	Method x	93(85)(59)	100 NA	[encodes 80% 8 15 31 32 40 48/ 24 25 52 54]	6 7 11 12 30 39 47/ 21 22 23 51 53
98.	Tg plant	59	80	8 15 31 32 40 48	-
99.	Tg plant	98(59)	100	8 15 31 32 40 48	-
100.	Tg plant	60	80	24 25	-
101.	Tg plant	100(60)	100	24 25	-
102.	Tg plant	63	80/80	8 15 31 32 40 48/ 24 25 52 54	-
103.	Tg plant	64	100/100	8 15 31 32 40 48/ 24 25 52 54	-

Claim	Type	Depends from	%ID	AA SEQ ID	NA SEQ ID
104.	Cereal	98(59)	80 AA	8 15 31 32 40 48	-
105.	Cereal	XXX			
106.	Cereal	100(60)	80 AA	24 25	-
107.	Cereal	XXX			
108.	Cereal	XXX			
109.	Cereal	XXX			
110.	Legume	98(59)	80 AA	8 15 31 32 40 48	-
111.	Legume	XXX			
112.	Legume	100(60)	80 AA	24 25	-
113.	Legume	XXX			
114.	Legume	XXX			
115.	Legume	XXX			
116.	Non-nod	98(59)	80 AA	8 15 31 32 40 48	-
117.	XXX				
118.	Non-nod	100(60)	80 AA	24 25	-
119.	XXX				
120.	XXX				
121.	XXX				
122.	AA	-	90 AA	52 54	-
123.	NA	122	90 AA	encodes 90%[52 54]	-
124.	Tg cell NA	122	90 AA	encodes 90%[52 54]	-
125.	Tg cell NA	124(122)	100 NA	Encodes 90% [52 54]	51 53
126.	Tg plant	122	90 AA	Encodes 90%[52 54]	-
127.	Tg plant	98(59)	80 AA	8	-
128.	Tg plant	98(59)	80 AA	15	-
129.	Tg plant	98(59)	80 AA	31	-
130.	Tg plant	98(59)	80 AA	32	-
131.	Tg plant	98(59)	80 AA	40	-
132.	Tg plant	98(59)	80 AA	48	-
133.	Tg plant	100(60)	80 AA	24	-
134.	Tg plant	59	100 AA	8	-
135.	Tg plant	59	100 AA	15	-
136.	Tg plant	59	100 AA	31	-
137.	Tg plant	59	100 AA	32	-
138.	Tg plant	59	100 AA	40	-
139.	Tg plant	59	100 AA	48	-
140.	Tg plant	60	100 AA	24	-
141.	Tg plant	122	100 AA	52	-

XXX=CANCELLED CLAIM

Claim 93 depends from claim 91

Claim 125 depends from claim 124